

SEARCH REQUEST FORM

52181

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up <u>10/3/01</u>	Bibliographic _____	Dr Link _____
Date Completed <u>10/5/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>04</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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2

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1      OPERATING SYSTEM:  PC-DOS/MS-DOS
2      SOFTWARE:  Patent Release #1.0, Version #1.30
3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER:  US/08/686,349
5      FILING DATE:
6      CLASSIFICATION:  435
7      ATTORNEY/AGENT INFORMATION:
8      NAME:  White, John P.
9      REGISTRATION NUMBER:  28,678
10     REFERENCE/DOCKET NUMBER:  0575/51731
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE:  (212) 278-0400
13     TELEFAX:  (212) 391-0525
14     INFORMATION FOR SEQ ID NO:  1:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH:  615 base pairs
17     TYPE:  nucleic acid
18     STRANDEDNESS:  single
19     TOPOLOGY:  linear
20     MOLECULE TYPE:  DNA (genomic)
21     HYPOTHETICAL:  NO
22     ANTI-SENSE:  NO
23     FEATURE:
24     NAME/KEY:  CDS
25     LOCATION:  1..615
26     US-08-686-349-1

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QY	421	AATTAAGCTACTTAAGACGCACTACAGATGTCACCCAAATTTGACCGCGCTATATTAGAGGAG	480
Db	421	AATTAAGCTACTTAAGACGCACTACAGATGTCACCCAAATTTGACCGCGCTATATTAGAGGAG	480
QY	481	CTTCAGGAGCTTAAGATATTGGGTGAGACACTTGTGCTTGAATTTATGTTCTGAGTGCATG	540
Db	481	CTTCAGGAGCTTAAGATATTGGGTGAGACACTTGTGCTTGAATTTATGTTCTGAGTGCATG	540
QY	541	GAAGAATTTGCAGAGTCGAAGCGCTCGGTTTGGACTATATCCGAGAGGTGACTCCGAGAC	600
Db	541	GAAGAATTTGCAGAGTCGAAGCGGTGCGTTTGGACTATATCCGAGAGGTGACTCCGAGAC	600
QY	601	GTCCACGATTAAG	612
Db	601	GTCCACGATTAAG	612

RESULT 2 4
US-08-686-349-1
: Sequence 1, Application US/08686349
: Patient No. 5861500
: GENERAL INFORMATION:
: APPLICANT: Chang, Yuan
: APPLICANT: Bohenzky, Roy A.
: APPLICANT: Russo, James J.
: APPLICANT: Edelman, Isidore S.
: APPLICANT: Moore, Patrick S.
: TITLE OF INVENTION: KAPOSI'S SARCOMA-ASSOCIATED HERPES VIRUS (KSHV)
: TITLE OF INVENTION: INTERLEUKIN 6 (IL-6) AND USES THEREOF
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

Query Match	100.0%	Score 612	DB 2	Length 615
Best Local Similarity	100.0%	Pred. No. 2,6e-201		
Matches 612	Conservative 0	Mismatches 0	Indels 0	Gaps
1	ATGTGCTGGTCAAGTTGGTCTCTCTGCGTGGTTCACGTGGTATCTGGAACG	60		
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61	CGGGGCAATTCGCCGAGCCGCCGAGTTGGAAAAGATCTTCTCATTTAGAGACTCAAT	120		
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121	TGAGTCTATGGGTGATGATGAATGCTCCGACCTCTGTACCGTACCGGACATTCGC	180		
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361	AACGTGAGACGATGAGACTCTCTGACGAAGACCTTAGATGGGACATACAGAAAGCTC	420		
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421	AATTAACCTACGTAACGACCTACAGCTCCAAATTTTGGAGGAGTATTAAGGAGAG	480		
421	AATTAACCTACGTAACGACCTACAGCTCCAAATTTTGGAGGAGTATTAAGGAGAG	480		
481	CTTCAGGAGACTTAAGTATTGGGTGAGACACTTGTCTGTTTATTTCTGAGTCAATG	540		
481	CTTCAGGAGACTTAAGTATTGGGTGAGACACTTGTCTGTTTATTTCTGAGTCAATG	540		
541	GAAATTTTGGAGGCTCAGCGCTGCTTTTGGAGCTCTATCCAGAGCTGACTCTGAC	600		
541	GAAATTTTGGAGGCTCAGCGCTGCTTTTGGAGCTCTATCCAGAGCTGACTCTGAC	600		
601	GTCACAGATTAAC 612			

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:51:09 : Search time 32.27 Seconds
(without alignments)
130.165 Million cell updates/sec

Title: US-09-230-048-2

Percent score: 1095
1 MCFKRLMSLLVCSILVSGT.....GQAVRVLDSIPPTDVRDK 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 segs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/CTUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	992	90.6	185	3	US-09-122-443-16
2	183.5	16.8	184	2	US-08-945-529-12
3	183	16.7	185	1	US-07-918-181A-4
4	183	16.7	185	1	US-07-918-181A-8
5	183	16.7	185	1	US-08-231-575-4
6	183	16.7	185	1	US-08-231-575-8
7	183	16.7	185	1	US-08-231-575-8
8	183	16.7	185	1	US-08-231-575-8
9	183	16.7	185	1	US-08-231-575-8
10	183	16.7	185	1	US-08-231-575-8
11	183	16.7	185	1	US-08-231-575-8
12	183	16.7	185	1	US-08-231-575-8
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25	183	16.7	185	1	US-08-231-575-8
26	183	16.7	185	1	US-08-231-575-8
27	183	16.7	185	1	US-08-231-575-8

28	181	16.5	185	2	US-08-766-620-5	Sequence 5, Appl
29	181	16.5	185	5	PCT-US93-06928-2	Sequence 2, Appl
30	181	16.5	185	5	PCT-US93-06928-6	Sequence 6, Appl
31	181	16.5	185	6	5186931-2	Patent No. 5186931
32	181	16.5	185	6	US-07-632-070B-2	Sequence 2, Appl
33	181	16.5	185	1	US-07-745-382-20	Sequence 20, Appl
34	181	16.5	185	1	US-07-921-848-20	Sequence 20, Appl
35	181	16.5	185	1	US-08-165-301A-20	Sequence 20, Appl
36	181	16.5	185	3	US-08-469-318-163	Sequence 163, App
37	181	16.5	185	3	US-08-468-609A-163	Sequence 163, App
38	181	16.5	185	4	US-08-810-436-20	Sequence 20, Appl
39	181	16.5	185	6	PCT-US94-14179-20	Sequence 20, Appl
40	181	16.5	185	5	PCT-US95-01185-163	Sequence 163, App
41	181	16.5	187	1	US-07-632-070B-3	Sequence 3, App
42	181	16.5	188	3	US-09-122-443-12	Sequence 12, App
43	181	16.5	317	3	US-08-469-318-145	Sequence 145, App
44	181	16.5	317	3	US-08-468-609A-145	Sequence 145, App
45	181	16.5	317	5	PCT-US95-01185-145	Sequence 145, App

ALIGNMENTS

```
RESULT 1
US-09-122-443-16
Sequence 16, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bajan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)456-1200
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-16
Query Match 90.6% Score 992 DB 3 Length 185
Best Local Similarity 100.0% Pred. No. 3.2e+11
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0
20 TGGKLPDAPPEEKDLLQRLNMLVWIDECFRLCYRTGICGKILEPAAIFHLKPAIND 79
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Db 1 TRGKLPDAFEKEDLLIQRNLNMLWVDECFRDLCTRTGICKGILEPAIFHLKLPALIND 60
QY 80 TDHCGIIGENENSCAKIADCFEEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEE 139
Db 61 TDHCGIIGENENSCAKIADCFEEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEE 120
QY 140 LNKLTTHSPKFRDGLGRGLGKLYVRRHFASFYVLSAMEKFAQAVRLSDIPDP 199
Db 121 LNKLTTHSPKFRDGLGRGLGKLYVRRHFASFYVLSAMEKFAQAVRLSDIPDP 180
QY 200 DVHDK 204
Db 181 DVHDK 185
RESULT 2
US-08-945-529-12
Sequence 12, Application US/08945529
Patent No. 5972902
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: PAONESSA, Giacomo
TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
TITLE OF INVENTION: THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,529
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000273
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT96/00084
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CILIBERTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-5528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-945-529-12
Query Match 16.8%; Score 183.5; DB 2; Length 184;
Best Local Similarity 27.4%; Pred. No. 3.3e-14;
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1;
QY 46 IDRCFRDL-----CRITGICGKILEPAIFHLKLPALINDHDCGLIGFNETSQL 94
Db 25 IDKQIDLDIFISLRKTCNKSNCESSEKADAFWNLNPKMAEKDCGFYKGFNETCL 84

QY 95 KKLADGFEFEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEELNKLTKTHSPKED 154
Db 85 VKIITGLFEFEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEELNKLTKTHSPKED 144
QY 155 RGLGRGLGKLYVRRHFASFYVLSAMEKFAQAVRL 191
Db 145 ASLITKLOANQWLODMTHLILRSKFEFLIRSLRAL 181
RESULT 3
US-07-918-181A-4
Sequence 4, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutains
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-918-181A-4
Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
QY 28 PEFEKDLIQRNLNMLWVDECFRDLCTRTGICKGILEPAIFHLKLPALINDHDCGLIG 87
Db 19 PLTSSERIDKQIRYILDIGISALRKTCNKSNCESSEKADAFWNLNPKMAEKDCGFOSG 78
QY 88 FNETSCIKKLAADGFEFEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEELNKLTKTH 147
Db 79 FNETCLVITITGLFEFEVYLFKLTTEREKSVINVDWMLLTKTIGNDIOEELNKLTKTH 138
QY 148 YSPKFRDGLGRGLGKLYVRRHFASFYVLSAMEKFAQAVRL 191
Db 139 TPDPTTNASLITKLOANQWLODMTHLILRSKFEFLIRSLRAL 182
RESULT 4
US-07-918-181A-8
Sequence 8, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.


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:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 185 amino acids
:      TYPE: amino acid
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
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US-08-231-575-8

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Query Match.	16.7%;	Score 183;	DB 1;	length 185;
Host Local Similarity.	25.6%;	Pred. No. 3.9e-14;		
Matches 42;	Conservative 38;	Mismatches 84;	Indels 0;	Gaps 0

QY 28 PEFENKOLLQRIANMNLAWYIDECFNDOLYRFGICKGLIEPAIFHLKLPINDTHICIG 87
 Db 19 PLTSSRIKQOIRYLIDGISAIRKRETCNKSMBESSKEALAEANNLPLPKMAKQDCPQSG 78
 QY 88 FNTSCKLRIAGPPEFPEYLFKPLTFTEGCKSVYINVDMMELTKTQIMDIJEBANKLRTH 147
 Db 79 FNETCLVAILITIGLEFVILEYIIONNFESSEBQARAYQMSKRVLLQFQKANKLDAIT 138
 QY 148 VSPRPEDRDLLOGLCKYWRWRHASTYVYSAMKFAAGAYRL 191
 Db 139 YPDPTTNASILTKRLOAQONQIMQDMTHLILKSLKEFQSGLRKL 182

RESULT 7
 PCT-US93-06928-4
 : Sequence 4, Application PC/TUS9306928
 : GENERAL INFORMATION:
 : APPLICANT: Fowlkes, Dana M.
 : TITLE OF INVENTION: Catboxy Terminal IL-6 MuteInfe
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Imclone Systems Incorporated
 : STREET: 180 Varlick Street
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 11014
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US93/06928
 : FILING DATE: 19930723
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/918,181
 : FILING DATE: 23-JUL-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Felt, Irving N.
 : REGISTRATION NUMBER: 28,601
 : REFERENCE/DOCKET NUMBER: POW-2-T
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212-645-1405
 : TELEFAX: 212-645-2054
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 185 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : PCT-US93-06928-4

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Query Match 16.7% Score 183 DB 5 Length 185
Best Local Similarity 25.6% Pred. No. 3.9e-14
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0
OY 28 PEFKKLLQRLMMWVIDECGRDLCYRTGICKILEPARIFFHLKLPAINDDHICLLS 87
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Db 19 PLESSERIDKQRYTILDIISALRKEFCNKNMSESKKVLAEENNLPRMAEKQCFQSG 78

Oy 88 FNESECLTKIADGFEPEFVLPKPLITTEGKGSYIVNVMETLTKTQWPIIOEENLKKRTH 147

Db 79 FNESETCLVAVITGLEPEVYIEVYIQNPNFSSFEQARAVQMSKRYLQIQLQKAKNDAIT 138

Oy 148 YSPKRFDRGLGRLGKLYWVRHAFSPYVLSAAEKRGAVNVL 191

Db 139 TPDPPTTNASTLTKIDQANQNMQIDMTTHLIRSLKEFVQSSALR 182

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      RESULT      8
PCT-US93-06928-8
: Sequence 8, Application PC/TUS9306928
: GENERAL INFORMATION:
: APPLICANT: Fomkes, Dana M.
: TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 11014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06928
: FILING DATE: 19930723
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/918,181
: FILING DATE: 23-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Felt, Irving N.
: REGISTRATION NUMBER: 28, 601
: REFERENCE/DOCKET NUMBER: FOM-2-T
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US93-06928-8

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Query Match	16.7%	Score 183;	DB 5;	Length 185;
Best Local Similarity	25.6%	Pred. NO. 3.9e-14;		
Matches 42;	Conservative 38;	Mismatches 84;	Indels 0;	Gaps 0

QY 28 PEFENKLLIQRINMMLAWIDCEFDICYPGICIGKGLFEALFHLKLAINDTHQCLIG 87
Db 19 PLTSSERIDKQIRYLIDISALRKETCNKSNMCESSEKALMANNINLPKMAEKDQCSFG 78
QY 88 FNTSCLKLADGFEFEFVLEKFLITECKSVINVDVMLLTKIGMDIOBELKKLRTKH 147
Db 79 FNEBCTLVKIIITGLLEFEFVLEYLATIONFESESOAANAOMSTRKVLIOPLQKAKNLAIT 138
QY 148 YSPKEDRGLLRGLQKTYWRHFASTYVUSAMETAGAVRL 191
Db 139 TPDPTMASLLTKLDAONQWIDQMTTHLLIRSLKEFMOSLLAL 182

RESULT 9
US-08-792-019B-9
; Sequence 9, Application US/08792019B

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Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9

Query Match      16.7% Score 183; DB 1; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

OY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLMWVIDECFRLCYRT 57
    :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 16 LGILLVLPAPAPAPPPGDSKDVAAAPRQPLTSSEIRIDKQIRYIIDGISALRKTCNKS 75
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 58 GICKGILPEPAIFHLKLAINDPDHCGLIGFNETSCCLKLADGFEFEVLFKPLTTEFGK 117
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 NMCKESKELAEENNLNLPKMAEKDCFGSFGNETCLVKITITGLFEFVYLELONRFES 135
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 118 SVINQVWMLLTGTLGMDIOELNKKIKRTHYSPKPRDGLIGRIQGLKTVRRHFAFVYL 177
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 136 SEQOAAAVQMSKVLIOELQKRNKNDLITPPPTNASLITKLOQONQMDMTHTLIL 195
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 178 SAMEKFAQAVFL 191
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 196 RSKREFLOSSRAL 209
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RESULT 10
US-08-988-819-9
Sequence 9, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
STATE: CA
```

```
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-988-819-9

Query Match      16.7% Score 183; DB 3; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

OY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLMWVIDECFRLCYRT 57
    :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 16 LGILLVLPAPAPPPGDSKDVAAAPRQPLTSSEIRIDKQIRYIIDGISALRKTCNKS 75
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 58 GICKGILPEPAIFHLKLAINDPDHCGLIGFNETSCCLKLADGFEFEVLFKPLTTEFGK 117
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 NMCKESKELAEENNLNLPKMAEKDCFGSFGNETCLVKITITGLFEFVYLELONRFES 135
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 118 SVINQVWMLLTGTLGMDIOELNKKIKRTHYSPKPRDGLIGRIQGLKTVRRHFAFVYL 177
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 136 SEQOAAAVQMSKVLIOELQKRNKNDLITPPPTNASLITKLOQONQMDMTHTLIL 195
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 178 SAMEKFAQAVFL 191
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 196 RSKREFLOSSRAL 209
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-016-534-9
Sequence 9, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
```

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: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/016.534
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/792.019
: FILING DATE: 03-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: COOK, ROBERT R.
: REGISTRATION NUMBER: 31,602
: REFERENCE/DOCKET NUMBER: A-442B
: INFORMATION FOR SEQ. ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..182
: NAME/KEY: Region
: LOCATION: -30..0
: US-09-016-534-9

Query Match      16.7%; Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTGKLPDAP-EFEKDL-----LIQRLNMMLWVIECFNDLCYRT 57
DB 16 LGLLLVPAFPAVPVPGEDSKVAAPIHROPITSSERIDKQIRYLIDGISALRETCNKS 75
QY 58 GICGCLIEPAIFHLKIPAIINDTHGCLIGFNETSCCLKIADGFEEFVLFKPLTFEFGK 117
DB 76 NMCCSSKEALAKENNLNPKMAEKDGCFOGCFNEETCLVKITGLLEFVLEYLQNFES 135
QY 118 SVINVDVMELLTTLGMDIOEELNKLTKTHYSPFKEDRGLGRLOGLKYNVRHFASFYVL 177
DB 136 SEQARAVQMSFTVLLQFLQKAKKNLDAITPPDPPTNNSLLTKLQAOQWLODMWTTHLL 195
QY 178 SAMEKFAQAVRYL 191
DB 196 RSFKEFLQSSLRAL 209

RESULT 12
US-08-097-869-7
: Sequence 7, Application US/08097869
: Patent No. 6204364
: GENERAL INFORMATION:
: APPLICANT: Todaro, George J.
: APPLICANT: Rose, Timothy M.
: TITLE OF INVENTION: HYBRID CYTOKINES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foxstar
: STREET: 545 Middlefield Road, Suite 200
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

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: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/097.869
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/753.178
: FILING DATE: 30-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24455-20001.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-813-5600
: TELEFAX: 415-327-2951
: TELEX: 706141
: INFORMATION FOR SEQ. ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-097-869-7

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Query Match      16.7%; Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTGKLPDAP-EFEKDL-----LIQRLNMMLWVIECFNDLCYRT 57
DB 16 LGLLLVPAFPAVPVPGEDSKVAAPIHROPITSSERIDKQIRYLIDGISALRETCNKS 75
QY 58 GICGCLIEPAIFHLKIPAIINDTHGCLIGFNETSCCLKIADGFEEFVLFKPLTFEFGK 117
DB 76 NMCCSSKEALAKENNLNPKMAEKDGCFOGCFNEETCLVKITGLLEFVLEYLQNFES 135
QY 118 SVINVDVMELLTTLGMDIOEELNKLTKTHYSPFKEDRGLGRLOGLKYNVRHFASFYVL 177
DB 136 SEQARAVQMSFTVLLQFLQKAKKNLDAITPPDPPTNNSLLTKLQAOQWLODMWTTHLL 195
QY 178 SAMEKFAQAVRYL 191
DB 196 RSFKEFLQSSLRAL 209

RESULT 13
US-08-795-473B-6
: Sequence 6, Application US/08795473B
: Patent No. 6217858
: GENERAL INFORMATION:
: APPLICANT: Galun, Eithan
: APPLICANT: Nahot, Orit
: TITLE OF INVENTION: A Pharmaceutical Composition for Treating
: TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Davidson and Kappel, LLC
: STREET: 1140 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS-DOS EDITOR
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795.473B

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FILED DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963,1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-795-4738-6

Query Match 16.7%; Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LQRLMMMLMWIDECFRDLCYRT 57
DB 16 LGLLLVLAAPAPVPPEGDSKDVAAHROPRTSSERIDKQIRYILDGISALRKETCNKS 75
QY 58 GICKGILPAAIFHLKLPAINDDHGLIGFNETSCLKIALDGFEFEVLEKFLTTERGK 117
DB 76 NMCSSKALAEENNINLPKMAEKDGCFOGPFNEETCLVKITGLLEFEVYLEYLNRRFS 135
QY 118 SVINVDWELLTKTLGMDIOELNKLTKTHYSPKRDGLGRLGSLGKXVHRHFAFVYL 177
DB 136 SEQARAVQWSTKYLIOFLQKAKNLDAITTPDPTNASLITKLAQNONQWLODMTHLIL 195
QY 178 SAMEKFAQAVRL 191
DB 196 RSKEFLQSSLRAL 209

RESULT 14
5510472-2
Patent No. 5510472
APPLICANT: REVEL, MICHEL; TIOUATS, PIERRE
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
INTERFERON-BETA2
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/883,633
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 208,925
FILING DATE: 20-NOV-1980
APPLICATION NUMBER: 449,447
FILING DATE: 12-DEC-1989
APPLICATION NUMBER: 860,883
FILING DATE: 08-MAY-1986
APPLICATION NUMBER: 208,925
FILING DATE: 20-NOV-1980
SEQ ID NO: 2
LENGTH: 212
5510472-2

Query Match 16.7%; Score 183; DB 6; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LQRLMMMLMWIDECFRDLCYRT 57
DB 16 LGLLLVLAAPAPVPPEGDSKDVAAHROPRTSSERIDKQIRYILDGISALRKETCNKS 75
QY 58 GICKGILPAAIFHLKLPAINDDHGLIGFNETSCLKIALDGFEFEVLEKFLTTERGK 117
DB 76 NMCSSKALAEENNINLPKMAEKDGCFOGPFNEETCLVKITGLLEFEVYLEYLNRRFS 135

QY 118 SVINVDWELLTKTLGMDIOELNKLTKTHYSPKRDGLGRLGSLGKXVHRHFAFVYL 177
DB 136 SEQARAVQWSTKYLIOFLQKAKNLDAITTPDPTNASLITKLAQNONQWLODMTHLIL 195
QY 178 SAMEKFAQAVRL 191
DB 196 RSKEFLQSSLRAL 209

RESULT 15
US-08-693-182-2
Sequence 2, Application US/08693182
Patent No. 5849283
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHN, Armin
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
SUPERAGONISTS, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
MODELING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A00805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CILIBERTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-182-2

Query Match 16.6%; Score 182; DB 2; Length 184;
Best Local Similarity 25.6%; Pred. No. 5.1e-14;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFEEDLQRLMMMLMWIDECFRDLCYRTGICKGILPAAIFHLKLPAINDDHGLIG 87
DB 18 PLTSSERIDKQIRYILDGISALRKETCNKSNCSSKALAEENNINLPMAEKDGCFOG 77
QY 88 PNETSCLKIALDGFEFEVLEKFLTTERGKSVINVDWELLTKTLGMDIOELNKLTKTH 147
DB 78 FNEETCLVKITGLLEFEVYLEYLNRRFSSSEQARAVQWSTKYLIOFLQKAKNLDAIT 137

Fri Oct 5 10:02:07 2001

us-09-230-048-2.raii

Page 8

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OY 148 YSPPKPGRGLCRLOGLKTWVRFPASTYVLSAMEKFAQAVRVL 191
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Db 138 TPDPPTNASLTKLQAGNQLQGMOTIHLIRSFEEGLSLRAL 181

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Search completed: October 4, 2001, 19:10:32
Job time: 1163 sec

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•
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•

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:48:59 : Search time 44.98 Seconds
(without alignments)
345.478 Million cell updates/sec

Title: US-09-230-048-2

Perfect score: 1095

Sequence: 1 MCFKMLSLVSGSLVSGT.....GQAVRVLDSIPDVTPEVHDR 204

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	183	16.7	212	1 IVHUB2	interleukin-6 prec
2	180.5	16.5	212	2 146530	interleukin 6 - pi
3	179.5	16.4	212	2 146621	prointerleukin 6 -
4	173.5	15.8	208	2 T09216	interleukin-6 prec
5	150	13.7	208	1 S29549	interleukin-6 - sh
6	148	13.5	211	1 ICMS6	interleukin-6 prec
7	143.5	13.1	208	1 A56610	interleukin-6 prec
8	134	12.2	211	2 A34247	interleukin-6 prec
9	128	11.7	207	2 146084	interleukin 6 - ca
10	86.5	7.9	487	2 H69477	coenzyme F420-gui
11	85	7.8	408	2 A56186	cyclin E - African
12	82.5	7.5	447	1 UBMDM	tubulin beta-1 cha
13	82.5	7.5	449	1 J01589	tubulin beta-5 cha
14	82.5	7.5	969	2 T41707	probable phenome
15	82	7.5	367	2 T18185	probable site-spec
16	81.5	7.4	442	2 S00683	tubulin beta-1 cha
17	80.5	7.4	444	2 J01581	tubulin beta-7 cha
18	80	7.3	955	2 F84972	valine-tRNA Lligas
19	79.5	7.3	451	2 S50748	beta-tubulin - pot
20	79.5	7.3	452	2 S50748	beta-tubulin - pot
21	79.5	7.3	1017	2 S67804	lmg1 protein - yea
22	79	7.2	385	2 T27626	hypothetical prote
23	78.5	7.2	445	2 JN0048	tubulin beta-1 cha
24	78.5	7.2	674	2 T19495	hypothetical prote
25	77.5	7.1	609	2 S04757	NADH dehydrogenase
26	77.5	7.1	771	2 S51421	hypothetical prote
27	77	7.0	1004	2 B69463	hypothetical prote
28	77	7.0	1810	2 T30562	resistance protein
29	76.5	7.0	447	2 S17729	tubulin beta chain

30	76.5	7.0	447	2 S17730	tubulin beta chain
31	76.5	7.0	461	2 T39889	protein kinase - f
32	76	6.9	1005	2 B82959	sarcosine oxidase
33	75.5	6.9	164	2 T32824	hypothetical prote
34	75.5	6.9	260	2 D64246	DNA-directed DNA p
35	75.5	6.9	602	2 H86579	DNA gyrase subunit
36	75.5	6.9	602	2 C72043	DNA gyrase subunit
37	75.5	6.9	1158	2 T50454	probable rho1 GDP-
38	75	6.8	172	2 A46695	epididymal secreto
39	75	6.8	172	2 A46695	ABC transporter, A
40	75	6.8	333	2 B64380	hypothetical prote
41	75	6.8	505	1 S19169	cytochrome P450 2D
42	75	6.8	524	2 T43050	cyclin E - Caenorh
43	75	6.8	570	2 T30156	hypothetical prote
44	74.5	6.8	227	2 A70357	hypothetical prote
45	74.5	6.8	399	2 A84475	hypothetical prote

ALIGNMENTS

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
C;Accession: A32648; A25692; A25696; A33515; A25801; A25921; I52193; I56003; A27601;
R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A;Reference number: A32648; MUID:88082664
A;Accession: A32648
A;Molecule type: DNA
A;Residues: 1-212 <TAB>
A;Cross-references: GB:Y00081; NID:929494; PIDN:CAA68278.1; PID:929495
R;Zilberstein, A.; Huggier, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a dI
A;Reference number: A91051; MUID:87053818
A;Accession: A25692
A;Molecule type: mRNA
A;Residues: 1-212 <TAB>
A;Cross-references: GB:X04430; NID:933673; PIDN:CAA28026.1; PID:932674
R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashim
I., T.; Kishimoto, T.
Nature 324, 73-76, 1986
A;Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
A;Reference number: A93387; MUID:87065033
A;Accession: A26966
A;Molecule type: mRNA
A;Residues: 1-212 <HIR>
A;Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
R;Tonouchi, N.; Mita, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 153, 1056-1062, 1989
A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A;Reference number: A33515; MUID:89391958
A;Accession: A33515
A;Molecule type: mRNA
A;Residues: 1-212 <TRON>
A;Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
R;Haegeman, G.; Content, J.; Voickeert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-637, 1986
A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A;Reference number: A25801; MUID:87004683
A;Accession: A25801
A;Molecule type: DNA; mRNA
A;Residues: 1-212 <HAEB>
A;Cross-references: GB:X04403
A;Experimental source: Fibroblast
R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
A:Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
A:Accession: A25921
A:Molecule type: mRNA
A:Residues: 1-212 <NAN>
A:Cross-references: GD:M4584; NID:9184628; PIDN:AAA5728.1; PID:9306910
R:Mong, G.G.; Mitek-Glanovotli, J.; Hewick, R.M.; Clarf, S.C.; Ogawa, M.
Hehring Inst. Molec. Biol. 83, 40-47, 1988
A:Title: Interleukin 6: identification as a hematopoietic colony-stimulating factor.
A:Accession: 152193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <MON>
A:Cross-references: GB:M54894; NID:9186351; PIDN:AAC41704.1; PID:9186352
R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
J. Immunol. 139, 4116-4121, 1987
A:Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
A:Reference number: 156003; MUID:88088768
A:Accession: 156003
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <NAN>
A:Cross-references: GB:M4403; NID:9184631; PIDN:AAA5729.1; PID:9306911
R:Van Damme, J.; Van Beaumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
J. Immunol. 140, 1534-1541, 1988
A:Title: Separation and comparison of two monokines with lymphocyte-activating factor activity
A:Reference number: A92815; MUID:8815445
A:Accession: A27601
A:Molecule type: protein
A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
A:Accession: B27601
A:Molecule type: protein
A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
R:Yamanoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, J.T.
J. Immunol. 144, 1808-1816, 1990
A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved in cell growth
A:Reference number: A60400; MUID:90171574
A:Accession: A60400
A:Molecule type: protein
A:Residues: 30-43 <VAM>
R:Hitano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and its cDNA
A:Reference number: A29085; MUID:87092370
A:Accession: A29085
A:Molecule type: protein
A:Residues: 29-42 <IIR>
R:Noda, M.; Takekda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Aizawa, Y.
Anticancer Res. 11, 961-968, 1991
A:Title: Purification and characterization of human fibroblast derived differentiation factor
A:Reference number: A61159; MUID:91290785
A:Accession: A61159
A:Molecule type: protein
A:Residues: 30-42 <MOD>
A:Experimental source: fibroblast
R:Ming, J.E.; Cornwell, C.; Stojman, R.M.; Cranneli-Pierro, A.
J. Mol. Cell. Immunol. 4, 203-212, 1989
A:Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for human myeloid leukemia cell lines
A:Reference number: A61462; MUID:90121567
A:Accession: A61462
A:Molecule type: protein
A:Residues: 28-48 <MIN>
A:Experimental source: leukocyte-conditioned medium
R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriske, J.B.; Sehgal, P.B.
Cytokine 3, 204-211, 1991
A:Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
A:Reference number: A48419; MUID:91355644
A:Accession: A48419
A:Molecule type: protein
A:Residues: 30-37, 'X', 39-40 <MAT2>
A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
A>Note: this 28-30k form contained both N-linked and O-linked carbohydrate; a 25k for

A:Accession: C4B619
A:Molecule type: protein
A:Residues: 28-40 <MAY>
A:Experimental source: FS-4 fibroblasts
A>Note: sequence extracted from NCBI backbone (NCBP:63787)
A>Note: this 23-25k form contained O-linked but not N-linked carbohydrate
R:Ortho: T.; Oheda, M.; Hasegawa, M.; Kubonikwa, H.; Esaki, K.; Ochii, N.
J Biochem 115, 345-350, 1984
A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
A:Reference number: JX0305; MUID:94266765
A:Contents: annotation, modified sites in recombinant protein from CHO cells
R:Clogston, C.L.; Boone, T.C.; Grandall, C.; Mendiaz, E.A.; Lu, H.S.
Arch. Biochem. Biophys. 272, 144-151, 1989
A>Title: Disulfide structures of human Interleukin-6 are similar to those of human gr
A:Reference number: S04981; MUID:89286115
A:Contents: annotation; disulfide bonds in recombinant protein
R:Rock, F.L.; Li, X.; Chong, P.; Iida, N.; Klein, M.
Biochemistry 33, 5146-5154, 1994
A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A:Reference number: A54253; MUID:94227044
A:Contents: annotation, lability and functional significance of each disulfide bond
C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
lolu lin secretion). It therefore appears to function as an autoregulator of cell grow
C:Comment: This protein plays a regulatory role in various host defense mechanisms an
C:Genetics:
A:Gene: CDB:116
A:Cross-references: GDB:120748; OMIM:147620
A:Map position: 7p21-7p21
A:Introns: 7/1; 70/3; 108/3; 157/3
C:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
F:1-27/Domin: signal sequence #status predicted <SIG>
F:28-212/Product: interleukin-6, long form #status experimental <MATL>
F:30-212/Product: interleukin-6, short form #status experimental <MATS>
F:72-78,101-111/Disulfide bonds: #status experimental
F:72/Binding site: carboxylate (asn) (covalent) (partial) #status experimental
F:166/Binding site: carboxylate (thr) (covalent) (partial) #status experimental
P:172/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 16.7%; Score 183; DB 1; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.4e-10;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

OY 12 VGSLLVSGTRGLPADP-EFEKDL-----LIQRLMMMLWVIDECFRDLCYRT 57
 ::||| ::||| ::||| ::|||
Db 16 LGILLVLPAFPAPVPPEGDSKDVAAPHROPLTSSERIDQIRYIIIDGISALRKETCKNS 75
OY 58 GICGLIEPAIFHLKLPAINDTHCGILIGENSTSCAKIADFFEEVLFKFLTERCK 117
 ::||| ::||| ::||| ::|||
Db 76 NMKESSKEALAEENNLMIPMAEKDCPCPSGNERTCLVKIITTLGEFVEYLLELDNRRFS 135
OY 118 SYINVDMELIKTKLGMDIOEELNKLIKTIHSPKEDRGILGLOGIKGVWRHFASFYVL 177
 ::||| ::||| ::||| ::|||
Db 136 SEBOARAVYMSIKRVLFLOFLKKAKNLDAITTPDTTNASLLTKLQANOMLQDMFTTHLL 195
OY 178 SAMEKFAQAVRVL 191
 ::||| ::||| ::||| ::|||
Db 196 RSKRFLOSSRL 209

RESULT 2
146590
Interleukin 6 - p19
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A>Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co
A:Reference number: 146590; MUID:92360284

RESULT
6
ICM56
Interleukin-6 precursor - mouse
N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte acyloma growth factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
A:Accession: A30571; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; R:Tanabe, O.; Akita, S.; Kamaya, T.; Wong, G.C.; Hirano, T.; Kishimoto, T.
J:Immunol. 141, 3875-3881, 1988
A>Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
A:Reference number: A30531; MUID:89035525
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <TAN>
A:Cross-references: GB:M20572; NID:g198369; PIDN:AAA3302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Sim
Eur. J. Immunol. 18, 193-197, 1988
A>Title: cDNA cloning of murine interleukin-6: homology with human interleukin 6.
A:Reference number: A27610; MUID:88166883
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-references: GB:M20572; NID:g52701; PIDN:CAA2960.1; PID:g52702
R:Mock, B.A.; Notzdan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
J. Immunol. 142, 1372-1376, 1989
A>Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOCK>
A:Cross-references: GB:M24221; NID:g341131; PIDN:AAAG814.1; PID:g870699
R:Stimpson, R.U.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A>Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
A:Reference number: S01323; MUID:88329059
A:Accession: S01323
A:Molecule type: protein
A:Residues: 25-166 /X/,168-211 <SIM>
A>Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-P
Nucleic Acids Res. 18, 6455, 1990
A>Title: Cloning and sequence analysis of the cDNA for murine Interleukin-6.
A:Reference number: S12103; MUID:91057159
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <RE>
A:Cross-references: EMBL:X54542; NID:S52727; PIDN:CAA3841.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Stimpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A>Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69 /X/,71-75;78-94;128-148 <AS>
R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoeve, C.; Coulie, P.G.; Rubira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A>Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
A:Reference number: A40486; MUID:89017145
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CH>
A:Cross-references: GB:J03783; NID:g198367; PIDN:CAA39301.1; PID:g309410
R:Shabo, Y.; Lotem, J.; Rudinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
Blood 72, 2070-2073, 1988

Title: The myeloid blood cell differentiation-inducing protein MGI-2A is Interleukin
Reference number: A60799; MUID:89062753

A:Accession: A60799
A:Molecule type: protein
R:Residues: 77-98 <SHA>
R:Blankenstein, T.; Old, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a
A:Reference number: S10241; MUID:90171860
A:Accession: S10241
A:Status: preliminary
A:Molecule type: DN
F:1.24 <BLA>
A:Residues: 1-6
A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CA35824.1; PID:g581860
Rizhang, J.G.; Reid, C.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
A:Title: Specific covalent modification of the tryptophan residues in murine Interleu
A:Reference number: S38254; MUID:94039075
A:Accession: S38254
A:Status: preliminary
A:Molecule type: protein
A:Residues: 38-60;75, 'X', 77-79,176-203 <ZHA>
C:Genetics:
A:Gene: 11-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokin
F:25-211/Product: Interleukin-6 #status experimental <MAY>

Query Match 13.5% Score 148; DB 1; Length 211;
Best Local Similarity 24.5%, Pred. No. 9,7e-07;
Matches 47; Conservative 35; Mismatches 96; Indels 14; Gaps 3;

OY 12 VGSILVSGT-----RGKL----PDAPFEKDLIQRIMNLWVIDECFIDLCTRTG 58
DB 15 LGMLVTTFATPSQVRGDPEDFTPRKPVTYSQVGLITHVLEIVEMRKELCNGNS 74
OY 59 ICKGLEPAIFPLKIIPAINPTDHGCLIGFMETGCLKIKNDGFPEVLFKFITTEF-GK 117
DB 75 DCMNDALAKENLKLPETQRNDGCIQTGYDEICLKLISGLLEHSHSYEKKNKKDN 134
OY 118 SVINVDYMEILLTKTGMDIQEELNKLTHTHSPPKFDRLGLGRLOGLKYWRHAFSFFYL 177
DB 135 KDKARAVLIQDDFTLLHFNFDEVKDLRKIVLPPTISNALTLDXLESQKEWLRTKTIOFIL 194
OY 178 SAMEKFGACAVR 189
DB 195 KSLEEFLKVTLR 206

RESULT 7
A: Accession: A56610
Interleukin-6 precursor - bovine
C: Species: Bos primigenius taurus (cattle)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C: Accession: A56610; S22162
R: Droommans, L.; Cludts, I.; Cleuter, Y.; Ketmann, R.; Burny, A.
A: Title: Nucleotide sequence of bovine Interleukin-6 cDNA.
A: Reference number: A56610; MUID:93076003
A: Accession: A56610
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-208 <ROS>
A: Cross-references: EMBL:X57317; NID:g2193; PIDN:CAA0572.1; PID:g2194
A: Experimental source: HIV induced B cell lymphosarcoma
A: Note: sequence extracted from NCBI backbone (NCBIRP.118917)
C: Superfamily: Interleukin-6
C: Keywords: cytokine

```

Query Match 13.1% Score 143.5; DB 1: Length 208;
Best Local Similarity 24.4%; Pred. No. 2.6e-06;
Matches 42; Conservative 37; Mismatches 86; Indels 7; Gaps 2;

Oy 20 TRCKLPDAPFEFKDLIQLRNLMLWIDECFRDLCYRTGICGKIGLEPAIFHLKPAIND 79
Db 41 TPRRLTLTPPEKTEALIKR---MVDKISAMRKEICEKNDCEBSKEFLANENLTPKME 97
Oy 80 TDRCGLIGFNETSCLEKLDADGFEFEVLEFKFLTEFGKSVINQVWMLTKTGMDIOBE 139
Db 98 KDCCFQSGFQACILRTTAGLEEQIYLDYLQNDYEDQENQVADLRKRNITLQILQK 157
Oy 140 LNKITHTHSPPKFDGGLGRLOGLKTYWRHFASTFYLSAMEKAGQAVL 191
Db 158 IADLT---PATNTDLKMOSSNEMVKNKAITILRLNLEPLOSIMAI 205

RESULT 8
A34247
Interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
J:Northmann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat Interleukin 6 gene and its expression in macrophage-derivative
A:Reference number: A34247; MUID:89380206
A:Accession: A34247
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1211 <NOR>
C:Cross-references: GB:M26744; NID:q204915; PIDN:AAA77659.1; PID:q204916
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 12.2% Score 134; DB 2: Length 211;
Best Local Similarity 23.7%; Pred. No. 2.1e-05;
Matches 47; Conservative 34; Mismatches 91; Indels 26; Gaps 4;

Oy 12 VGLSLVSGT-----RGLPDAPFEKDLIQR-----LNMLWIDECFRD 52
Db 15 LGMLLATPAPFTPSQVRG-----DFTEDTHNHPVYTSQVGLITTYLREILMRKE 68
Oy 53 LCYRTGICGKIGLEPAIFHLKPAINDHCGLIGFNETSCIKRLADGFEFEVLEFKFLT 112
Db 69 LCNNSQNSMDSALSENMLKPEIQRNDGCGQGYNGEILCLIKGGLLEFFFLFYK 128
Oy 113 TEFGRKVINQVWMLTKTGMDIOBELNKITHTHSPPKFDGGLGRLOGKLYWRH 171
Db 129 NNLQDNKKDKARVIGSTPELVHFRQEKIDSYKIVLPTPSNALMEKLESQEWLRL 188
Oy 172 ASFYVLSAMEKFAQAVR 189
Db 189 TIQLITKALEEFLKVTMR 206

RESULT 9
146084
Interleukin 6 - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I46084
R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A:Title: Molecular cloning and characterization of a cDNA encoding feline Interleukin-6
A:Reference number: I46084; MUID:94052249
A:Accession: I46084
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: mRNA
A:Residues: 1-207 <BRA>

```

C:\Cross-references: GB:Lt6914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C:\Superfamily: Interleukin-6

```
Query Match          11.7%; Score 128; DB 2; Length 207;  
Best Local Similarity 27.8%; Pred. No. 7.7e-05;  
Matches   42; Conservative    29; Mismatches   62; Indels   18; Gaps   5;
```

OY 4 FKLSLLV-----GSLVSSTGRKLPDPEFEKDILLIQRNMMLWVIDECRDICVR 56
| | : || | | | | :|| | | | | | | | | | | | | | | |
Db 14 FSLGLLVATAPPTGPPLGGDATSNRLPPLR---ADKMELIKYLIGKSALKRMCMCN 70
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 57 TGICKLLEPAALFHLKPAINDTDHCGLGNETSCKLKLAQDFEEVLKEFLTETRE 115
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 71 YNKCEDEKEMIAENNINLPKLAEKDGCFOSSGNDETCLTRITTCGLAEOFYILKFLODKYE 130
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 116 ----GKSV-INVDVMELLTKTGMDIOEEL 140
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131 GDKNAKSYVTSTNYTLQMHLKRKKKN-QDEV 160

RESULT 10
H69477
cenzymase f420--guanine oxidoreductase [EC 1.6.5.-] 53.9k chain AFI825 [similarity]
N Alternate names: f420OH2-guanine oxidoreductase, 53.9k subunit nuoM homolog
C Species: Archaeoglobus fulgidus
C Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C Accession: H69477
R Klein, R.P., Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A Authors: Ullrichack, T.; Cotton, M.C.; Spriggs, T.; Attiach, P.; Kayne, B.P.; Sykes,
Smith, H.O.; Moese, C.R.; Venter, J.C.
A Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archael
C Reference number: A69250; MUID:98049343
Accession: H69477
A Status: preliminary; nucleic acid sequence not shown; translation not shown
A Molecule type: DNA
A Residues: 1..487 <FILE>
A Cross-references: GB:AEO00976; GB:AEO00782; NID:92669299; PIDN:AA8B9424.1; PID:92664
C Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C Keywords: oxido-reductase

Query Match 7.9%; Score 86.5; DB 2; Length 487;
Best Local Similarity 21.4%; Pred. No. 1.9;
Matches 48; Conservative 40; Mismatches 79; Indels 57; Gaps 12;

OY 4 FKLSLLVGSILAASGRRKLP-----DADEFEKDLL----IORLNMMML----- 43
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 FTAMLLIFLMIV-----KIQLGPHIMLPMAHAEPAPSALLSPLYAGLAGYULAV 262
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 44 WVIDECR-----ROLCTRTGICGLEPPAILFKLRPAINDTDHCGLGFNETS----- 92
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 263 YMIDSSEIDQRYRIIIAYAVISIYAQSFSVKOK-----DYRKLIAYSTSOMGYULL 315
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 93 -----CDKTAKADFEEVEVFKELTTERGSKSIYNDDVELMTTKTLGMDOIELNTKTHTVS 149
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 316 ALCL-----SGYGILLGVVIQVISAHARKSLTEFTACAIIASIRHG---LRDNRSRGHEEV 368
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 150 PKFRDRGLG-RLOGIKTYWRHFASFVYLASMEEKFAOAQAVRV 191
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 369 PTIANMALGTGMTLSGI-LTIIGNFGEFYIAGLTITIYGFNLAVI 411

RESULT 11
A56186
cyclin E - African clawed frog
N Alternate names: cyclin EI
C Species: Xenopus laevis (African clawed frog)
C Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jul-1999
C Accession: A56186; S34125

R:Rempel, R.E.; Sleight, S.B.; Møller, J.L.
 J. Biol. Chem. 270, 6843-6855, 1995
 A>Title: Maternal Xonopus Cdk-cyclin B complexes function during meiotic and early embry
 A:Reference number: A56186; M0ID:9520484
 A:Accession: A56186
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-408 <REM>
 A:Cross-references: GB:123857; NID:9431745; PIDN:AAA73524.1; PID:9431746
 R:Contulter, A.; Philippe, M.
 submitted to the EMBL Data Library, June 1992
 A:Description: Cloning and expression of Xonopus cyclin E.
 A:Reference number: S34125
 A:Accession: S34125
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-32, 'A', 34-199, 'NV', 202-258, 'GN', 261-408 <COU>
 A:Cross-references: EMBL:213966
 C:Superfamily: cyclin
 C:Keywords: cell cycle control

Query Match 7.8%; Score 85; DB 2; Length 408;
 Best Local Similarity 23.9%; Pred. No. 2.2;
 Matches 37; Conservative 29; Mismatches 41; Indels 48; Gaps 10;

OY 28 PEPEKDLIQLRLNMLVDECPRLCYRTGIC---KGILEPAIFHLKLPAINDTDHC 83

DB 267 PQPQELIYD---IVQLDLCVLDIC---CLEPYGVLAASMYFSPBELYK--- 314

OY 84 GLIFNET---SCLKLADGFEFEVLEFKLTTERKSVIN---VDV----- 124

DB 315 -VSGFKYTELQCCIKWL-----VYFMAAIKEGKSKLNFPGVDEAHNIOTHSQC 365

OY 125 MRLTKT-LQMDIQEELNKLWKTH---YSPKFRD 155

DB 366 LELMEKYVINOALLEQONRTSPICVLTLPQSNK 400

RESULT 12

UBMDBM tubulin beta-1 chain - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999

C:Accession: J02775

R:Oppenheimer, D.G.; Haas, N.; Silflow, C.D.; Snustad, D.P.
 Gene 63, 87-102, 1988

A>Title: The beta-tubulin gene family of Arabidopsis thaliana: preferential accumulation

A:Reference number: J02775; M0ID:88253862

A:Accession: J02775

A:Molecule type: DNA

A:Residues: 1-2447 <OPP>

A:Cross-references: GB:M20405; NID:9166921; PIDN:AAA32893.1; PID:9166922

A>Note: the genome of A. thaliana contains a beta-tubulin gene family consisting of 12

A:Genetics: the transcript of this beta-1 tubulin gene accumulates predominantly in roots

A:Interons: 133/1, 223/1

C:Superfamily: tubulin

C:Keywords: microtubule

F:141-147/Region: tubulin/Flaz GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

Query Match 7.5%; Score 82.5; DB 1; Length 447;
 Best Local Similarity 23.8%; Pred. No. 4.2;
 Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

OY 12 VGSLLVSGTRGKLPD-----APEPEKDLIQLRLNMLV-----IDEC----- 49

DB 148 MCTLLISKIEEYVDRMLTFVSFSPKV-SPTVVEPYNATLSYQLVENADCEMVDNE 206

OY 50 -FRDLCTRTGICGILEPAIFHLKLPAINDTDHCGLGFPNTSG-----LKL 97

DB 207 ALDYICRT-----LKLSTPSRGDLNHLISMTSGVTCSLRFGQLNSDLRL 254

OY 98 ADGFEFEVLEFK-----LTTEFGKSVINDVMELTKTGLMD 135

DB 255 AVNLIPEPRHLFFWVGAPLTSNGSOQYISLTVPELTQOM--WD 296

RESULT 13

J01589 tubulin beta-5 chain - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 13-Aug-1999

C:Accession: J01589

R:Snustad, D.P.; Haas, N.A.; Kopecek, S.D.; Silflow, C.D.
 Plant Cell 4, 549-556, 1992

A>Title: The small genome of Arabidopsis contains at least nine expressed beta-tubul

A:Reference number: J01587; M0ID:92361268

A:Accession: J01589

A:Molecule type: DNA

A:Residues: 1-449 <SNU>

A:Cross-references: GB:M84702; NID:9166901; PIDN:AAA32883.1; PID:9166902

C:Genetics:

A:Gene: TUB5

C:Superfamily: tubulin

C:Keywords: microtubule

Query Match 7.5%; Score 82.5; DB 2; Length 449;
 Best Local Similarity 23.8%; Pred. No. 4.2;
 Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

OY 12 VGSLLVSGTRGKLPD-----APEPEKDLIQLRLNMLV-----IDEC----- 49

DB 148 MCTLLISKIEEYVDRMLTFVSFSPKV-SPTVVEPYNATLSYQLVENADCEMVDNE 206

OY 50 -FRDLCTRTGICGILEPAIFHLKLPAINDTDHCGLGFPNTSG-----LKL 97

DB 207 ALDYICRT-----LKLSTPSRGDLNHLISMTSGVTCSLRFGQLNSDLRL 254

OY 98 ADGFEFEVLEFK-----LTTEFGKSVINDVMELTKTGLMD 135

DB 255 AVNLIPEPRHLFFWVGAPLTSNGSOQYISLTVPELTQOM--WD 296

RESULT 14

T41707 probable pheromone response zinc proteinase (EC 3.4.24.-) - fission yeast (schizosacc

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000

C:Accession: T41707

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1998

A:Reference number: 222011

A:Accession: T41707

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-969 <MUR>

A:Cross-references: EMBL:AL031180; PIDN:CAA20142.1; GSPDB:GM00066

A:Experimental source: strain 972h; cosmid c2E11 -chimeric

C:Genetics:

A:Gene: SPAC2E11.12c

A:Map position: 1

C:Superfamily: Insulin

C:Keywords: hydrolase; metalloproteinase; zinc

F:68/72/Binding site: zinc (His) #status predicted

F:71/Active site: Glu #status predicted

Query Match 7.5%; Score 82.5; DB 2; Length 969;
 Best Local Similarity 24.3%; Pred. No. 10;
 Matches 46; Conservative 24; Mismatches 64; Indels 55; Gaps 10;

OY 15 LVSGTRGKLPDAPPEPEKDL-----LIQRLNMLVINDCEPRDLCTRTGICGT 63

Db 73 LLMWGR-KYPDENRYKYLESHINGISNATASNTNTNYF-----EVSIDALY-----GA 121

Qy 64 LEPALIFHL-----KLPAINDTHCGCLIGFNEWISCKLADGFEFEVLFKFLT 112

Db 122 LDRFAQFIDPLFLECKDRIEIRAV-DSEK-----KNQDSMRFRMLRYSVLS 169

Qy 113 TERGKSVI-----NVDMELLTYLTSLMDQLELNLKLTTHYSPPKFRDGLGR-LQGL 164

Db 170 NP--KVSFSPKFTNGTIFETLGVPREGLDVRQELKFDYKYSANIMRLVIGREPIDVL 227

Qy 165 KYVWRHFA 173

Db 228 QDMAAELEFS 236.

RESULT 15

C:Probable site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Chlorella
 C:Species: Chlorella virus PCV-1
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18185
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T18185
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-367 <GRA>
 A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC6987.1
 A:Experimental source: specific host Chlorella strain NC64A
 C:Genetics:
 A:Note: A683L
 C:Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII
 C:Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match	7.58;	Score 82;	DB 2;	Length 367;
Best Local Similarity	26.0%;	Pred. NO. 3.7;		
Matches	32;	Conservative	19;	Mismatches 48;
				Indels 24;
				Gaps 3;

[illegible]

Search completed: October 4, 2001, 19:09:51
Job time: 1252 sec

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DB 16 LGLLVLPAAFPAPVLPGEEDSKDVAAPHISOPLTSSRIDKNIIRYILDDGISALRKETGNS 75
 OY 58 GICGILEPAAIFHLKPAINDYDHGCLIGFNETSCLKLADGFEFEVLFKPLTTEFGK 117
 DB 76 NMCSSKSEALAEENLNLPKMAEKDGCFOGSEFNDCLVYITGLLEFEVLEYLYQNRFES 135
 OY 118 SVINVDWEILTKTIGMDIOEELNKLTKTHYSPKFRDGLGRLOGLKRYWRHFAFVYL 177
 DB 136 SEQDRAVQMSKTLYLOLQKKAKNDATITPEPTTNASLTKLQANQMLQDMTHLIL 195
 OY 178 SAMEKFAQAAYRVL 191
 DB 196 RSFKEFLQSSLRAL 209

RESULT 2

IL6_CERTO 2
 ID IL6_CERTO STANDARD: PRT: 212 AA.
 AC P46650;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Cercopithecus torquatus alyx (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_Taxid=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJ;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayo A.E., Chikala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 RT nonhuman primates";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC -----
 CC EMBL: L26032; AAA9972.1; .
 DR HSSP: P05231; IALU.
 DR InterPro: IPR001716; .
 DR Pfam: PF00489; IL6_1.
 DR PRINTS: PRO0433; IL6CSFNG.
 DR PRINTS: PRO0434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT CARBOHYD 101 111 POTENTIAL.
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 212 AA; 23668 MW; C73C035226B4B9F CRC64;

OY 12 VGSLLVSTGRGLPDAP-EFEKDL-----LTIORLMMWIMYIDECFRDLCYRT 57
 DB 16 LGLLVLPAAFPAPVLPGEEDSKDVAAPHISOPLTSSRIDKNIIRYILDDGISALRKETGNS 75
 OY 58 GICGILEPAAIFHLKPAINDYDHGCLIGFNETSCLKLADGFEFEVLFKPLTTEFGK 117
 DB 76 NMCSSKSEALAEENLNLPKMAEKDGCFOGSEFNDCLVYITGLLEFEVLEYLYQNRFES 135
 OY 118 SVINVDWEILTKTIGMDIOEELNKLTKTHYSPKFRDGLGRLOGLKRYWRHFAFVYL 177
 DB 136 SEQDRAVQMSKTLYLOLQKKAKNDATITPEPTTNASLTKLQANQMLQDMTHLIL 195
 OY 178 SAMEKFAQAAYRVL 191
 DB 196 RSFKEFLQSSLRAL 209

RESULT 3

IL6_HUMAN
 ID IL6_HUMAN STANDARD: PRT: 212 AA.
 AC P05231;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
 GN IL6 OR IFNB2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87065033; PubMed=3491322;
 RA Hirano T., Yasukawa K., Harada H., Taga T., Matsuda T.,
 RA Kashiwamura S.-I., Nakajima K., Koyama K., Iimatsu A., Tanasawa S.,
 RA Saito Y., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 RT "Complementary DNA for a novel human Interleukin (BSF-2) that induces
 RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Matsuda T.,
 RA Nakai S., Kishimoto T.;
 RT "Structure and expression of human B cell stimulatory factor-2
 RT (BSF-2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helgott D.C., Sehgal P.B.;
 RT "Anti-beta-Interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts;
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87053818; PubMed=3023045;
 RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
 RT "Structure and expression of cDNA and genes for human
 RT Interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBO J. 5:2529-2537(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88088768; PubMed=3320204;
 RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.;
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [6]

Query Match 16.7%; Score 183; DB 1; Length 212;
 Best Local Similarity 26.3%; Proc No. 1.8e-10;
 Matches 51; Conservative 35; Mismatches 94; Indels 14; Gaps 2;

RP SEQUENCE FROM N.A. Pubmed-2789513;
 RA MEDLINE-89391958; Pubmed-2789513;
 RA Tonouchi N., Mima K., Karsayama H., Matsui H.;
 RT "Detection of 3' untranslated region of human Bst-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells."; Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RP [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE-87004683; Pubmed-3758081;
 RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Fiers W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts."; Eur. J. Biochem. 159:625-632(1986).
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-8919317; Pubmed-3266463;
 RA Wong G., Mitek-Giamotti J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor."; Behring Inst. Mitt. 83:40-47(1988).
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [9]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93178270; Pubmed-1291290;
 RA Chen O.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer."; Chung-Hua Chung Lin Tsa Chih 14:340-344(1992).
 RL Chung-Hua Chung Lin Tsa Chih 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RA MEDLINE-88154445; Pubmed-3279116;
 RA Van Damme J., Van Beeumen J., Decock B., Van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6."; J. Immunol. 140:1534-1541(1988).
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RA MEDLINE-95154344; Pubmed-7851440;
 RA Breton J., la Flura A., Bertolero F., Orsini G., Valsassina B.,
 RA Ziliotto R., de Filippis V., Polverino de Lauro P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond."; Eur. J. Biochem. 227:573-581(1995).
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RA MEDLINE-89286115; Pubmed-2472117;
 RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor."; Arch. Biochem. Biophys. 272:144-151(1989).
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MUTAGENESIS.
 RA MEDLINE-91243808; Pubmed-2037043;
 RA Letticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6."; FEBS Lett. 282:265-267(1991).
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96134845; Pubmed-8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy."; Biochemistry 35:273-281(1996).
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97303053; Pubmed-9159484;

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RT "Solution structure of recombinant human interleukin-6."; J. Mol. Biol. 268:468-481(1997).
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97224126; Pubmed-9118960;
 RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of interleukin 6: implications for a novel
 RT mode of receptor dimerization and signalling."; EMBO J. 16:989-997(1997).
 RL EMBO J. 16:989-997(1997).
 RN [17]
 RP FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 DR EMBL: X04430; CAA28026.1; -
 DR EMBL: M14584; AAA52728.1; -
 DR EMBL: X04602; CAA8268.1; -
 DR EMBL: Y00081; CAA68278.1; -
 DR EMBL: M18403; AAA52729.1; -
 DR EMBL: M29150; AAA59154.1; -
 DR EMBL: X04402; CAA27990.1; -
 DR EMBL: X04403; CAA27991.1; -
 DR EMBL: M54894; AAC41704.1; -
 DR EMBL: S56882; AAC13886.1; -
 DR EMBL: A09363; CAA00839.1; -
 DR PIR: A13248; IVH0B2.
 DR PIR: A25921; A25921.
 DR PDB: 1IL6; 04-FEB-98.
 DR PDB: 2IL6; 04-FEB-98.
 DR PDB: 1ALU; 03-JUN-98.
 DR MIM: 147620; -
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMCP.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
 FT FT SIGNAL 1 29
 FT CHAIN 1 30 212
 FT DISULFID 72 78 INTERLEUKIN-6.
 FT DISULFID 101 111
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .).
 FT MUTAGEN 173 173 A->V: ALMOST NO LOSS OF ACTIVITY.
 FT MUTAGEN 185 185 W->R: NO LOSS OF ACTIVITY.
 FT MUTAGEN 204 204 S->E: 13% ACTIVITY.
 FT MUTAGEN 210 210 M->T,N,S,R: LOSS OF ACTIVITY.
 FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
 SQ SEQUENCE 212 AA: 23718 MW: 17151 Da IPIEDIFELV734079 CRG64;
 Query Match 16.7%; Score 183; DB 1; Length 212;
 Best Local Similarity 25.8%; Pred. No. 1.8e-10;
 Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
 Oy 12 VGSILVSGTRKGLPAP-PFENDL-----LIQRIMMLAVIDECDRCDCRYET 57
 Db 16 LGLILVLPAPFPVPPGDSKDVAPAPRPLTSSERIDQIRILDLGSLARKKRCNKS 75
 Oy 58 GICKGILPEPAIFHLKLPAINDTDHCGLIGFNESCILKLADGFFFEVLPFKPLTFEPCK 117
 Db 76 NMCESSKEALAEENLNLPAPMAEKDCGFSQFNNEECVAKITGILFEVYLIVLQNRFS 135

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OY 118 SVINVDVMEELTKTGMDIOELNKLTKTHYSPKEDRGLGRLOGLAKYWRHFAFVYL 177
DB 136 SEEGARAVQWSTKVLIOFLQKAKNLDATITTPPTTNASLLTKLOAONOMLODMTHIL 195
OY 178 SMEKEFGQAVRVL 191
DB 196 RSFEKFELOSILRAL 209

RESULT 4
IL6_MACMU STANDARD; PRT; 212 AA.
ID IL6_MACMU
AC P51494.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2.
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brer S.S., Mayne A.E., Chikale N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 153:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HIPPOCAMPUS IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL: L26028; AAA99978.1; -
DR HSSP: P05231; IALU.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6CSFMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT SEQUENCE 212 AA; 23728 MW; 4130DEF0CBCCAD CRC64;

Query Match 16.5%; Score 161; DB 1; Length 212;
Best Local Similarity 25.5%; Pred. No. 2,8e-10;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;
OY 4 PKLWSLLVLSL-----LVSGTRGKLPDAPFE-----KDLILQRLMMIMLVIDECPDLCY 55
DB 14 FSLGLLVLPAAFPAPVLPCEDESKNAAPHSQPLTSSERIDKHIVLUDGISALRKETCN 73
OY 56 RTGCKGILBPAIFHLKLPAINDTDHGCLIGFNETSCLKLADGFEFEVLFKFLTTF 115

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DB 74 RSNKESSEKALNENNLTKPMKMKDCCFGSGNEDTCLVKITITGLLEFVYELQNR 133
OY 116 GKSVINVDVMEELTKTGMDIOELNKLTKTHYSPKEDRGLGRLOGLAKYWRHFAFVYL 175
DB 134 ESSEGARAVQWSTKVLIOFLQKAKNLDATITTPPTTNASLLTKLOAONOMLODMTHIL 193
OY 176 VLSAMEKFGQAVRVL 191
DB 194 ILRSFEKFELOSILRAL 209

RESULT 5
IL6_PIG STANDARD; PRT; 212 AA.
ID IL6_PIG
AC P26893.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9338547; PubMed=1873476;
RA Richards C., Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
RT expression of mRNA in synovial fibroblasts in vitro."
RL Cytokine 3:269-276(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92360284; PubMed=1497880;
RA Matchalagan N., Bixby J.A., Roberts M.R.;
RT "Expression of interleukin-6 in porcine, ovine, and bovine
RT preimplantation conceptuses."
RL Mol. Reprod. Dev. 32:324-330(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HIPPOCAMPUS IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M86722; AAC3733.1; -
DR EMBL: M80258; AAC27127.1; -
DR HSSP: P05231; IALU.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6CSFMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CONFLICT 30 30 G -> E (IN REF. 2).
FT SEQUENCE 212 AA; 23880 MW; EF100ED030B6DD0 CRC64;

Query Match 16.4%; Score 179.5; DB 1; Length 212;
Best Local Similarity 23.9%; Pred. No. 3,8e-10;

```



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CC -----
DR EMBL: L16914; AAA16630.1;
DR EMBL: D13227; BAA02507.1;
DR HSP: P05231; IL6;
DR InterPro: IPR001716;
DR Pfam: PF00489; IL6;
DR PRINTS: PR00433; IL6CSFNGF;
DR PRINTS: PR00434; INTERLEUKIN_6;
DR PROSITE: PS00254; INTERLEUKIN_6;
DR CYOKINE: Glycoprotein; Growth factor; Signal.
KM SIGNAL 1 27
FT CHAIN 28 208
FT DISULFID 68 74
FT DISULFID 97 107
FT CONFLICT 2 2
FT CONFLICT 45 45
FT CONFLICT 133 133
FT CONFLICT 173 187
FT CONFLICT 200 201
FT SEQUENCE 208 AA; 23401 MW; 93B4456B2989CAAC CRC64;

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Query Match 14.9%; Score 163.5; DB 1; Length 208;
Best Local Similarity 26.8%; Pred. No. 1.3e-08;
Matches 55; Conservative 39; Mismatches 84; Indels 27; Gaps 7;

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QY 4 FKLMSLLV-----GSLVSGTRGKLPDAFEKDLILQRLNMLNVIDECPRDLCYR 56
DB 14 FSLGLLVVTAFTPPGPGDQATSNRPULT---SADNMEELLYILGKLSALKREKCDN 70
QY 57 TGICGILPEPAIFHLKLPAINDPDHCGLGFNETSCGLKADGFEFEVLFKFLTEFG 115
DB 71 YNCKDESEALAEENNLNLPKLAEDGCFQSGFNQETCLRTTGLLEFOIHLKQANYEG 130
QY 116 -----CKSV-INDVMEELITGLDIOBELNKLTKHTYSPKPKDGLGRLGCKYWR 159
DB 131 GDEENAKSVTSTNVLQMLKRRKKN-QDEV-----IPVPEVGLQAKLOSQEBMLR 183
QY 170 HFASFVYLAME--KFAQAVRVL 191
DB 184 HTHTLTLRLIEDPLQPSLRVAVIM 208

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RESULT 8

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ID IL6_PROVI STANDARD: PRT: 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plinipedis; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Scott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----

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DR EMBL: I46802; AAB01430.1;
DR HSP: P05231; IL6;
DR InterPro: IPR001716;
DR Pfam: PF00489; IL6;
DR PROSITE: PS00254; INTERLEUKIN_6;
DR CYOKINE: Glycoprotein; Growth factor; Signal.
KM SIGNAL 1 1
FT CHAIN 27 209
FT DISULFID 69 75
FT DISULFID 98 108
FT SEQUENCE 209 AA; 23483 MW; 7514922E43B48B9 CRC64;

```

```

Query Match 14.6%; Score 159.5; DB 1; Length 209;
Best Local Similarity 22.8%; Pred. No. 3.1e-08;
Matches 45; Conservative 45; Mismatches 90; Indels 17; Gaps 3;

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```

QY 12 VGSLSVSGTRGKLP-----DA-----PEFEKDLILQRLNMLNVIDECPRDLCYR 57
DB 13 LGILLVAVTAFTPPGPGVGEQADATSNRPULTSPDKMEERIKYLSALKREKCDKY 72
QY 58 GICGILPEPAIFHLKLPAINDPDHCGLGFNETSCGLKADGFEFEVLFKFLTEFGK 117
DB 73 NKCEDESEALAEENNLNLPKLAEDGCFQSGFNQETCLRTTGLLEFOIHLKQANYEG 132
QY 118 SVINDVMEELITGLDIOBELNKLTKHTYSPKPKDGLGRLGCKYWRHFASTYVL 177
DB 133 NKEANSVYSTRLVQMLKRRKKNQDEVTPPTDTSLOALIKADCKMLKHTHTLIL 192
QY 178 SAME--KFAQAVRVL 191
DB 193 RSLIEDPLQPSLRVAVIM 209

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RESULT 9

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ID IL6_ORCOR STANDARD: PRT: 205 AA.
AC Q28747;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN Orcinus orca (killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Scott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.

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CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: LA6803; AAB01429.1; -.
DR HSSP: P05231; IL6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21
FT NON_TER 1 1
FT CHAIN 22 205
FT DISULFID 64 70
FT DISULFID 93 103
FT CARBOHYD 164 164
SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;
Query Match 14.2%; Score 155.5; DB 1; Length 205;
Best Local Similarity 21.1%; Pred. No. 7.3e-08;
Matches 42; Conservative 46; Mismatches 96; Indels 15; Gaps 3;
QY 8 SLLVGSLLVSTGRGLPD--APEFENDLIGRL-----NMMLWVDECFRL 53
D 4 SAEISGLLVTAATPEGLPEDEKDDTSRLYLSPKTEALIKYILGKISAMRKEM 63
QY 54 CVRTGICGKILEPAAIFHLKLPALNDHDCGLGFENSTGLKRLADGFEFEVLEFRL 113
D 64 CEYKCKENSKALLENMLNPKEAKDGCQSGFNQETLMTITGLLEYQYLDYLD 123
QY 114 EFGKSYINVDVNEILLTKLGMIDQELNKLTKTHYSPPKDRGLGLGKLVYVHRPA 172
D 124 EYEGDKAEALVAQVSISSKLAQTLRKQVKNPDEVTPPTTNASIMNMLNLSQNDMMKNTK 183
QY 173 SFYVLAMERKFAQAVRL 191
D 184 IILLRSLENFLQFSIRAI 202
DB
RESULT 10
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC 028319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97392354; Pubmed-9250586;
RT Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells."
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----
DR EMBL: D86569; BAA13118.1; -.
DR HSSP: P05231; IL6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6CSFNGF.
DR PROSITE: PS00434; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29
FT CHAIN 30 208
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 38 38
SQ SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;
Query Match 13.9%; Score 152; DB 1; Length 208;
Best Local Similarity 26.2%; Pred. No. 1.6e-07;
Matches 37; Conservative 31; Mismatches 69; Indels 4; Gaps 1;
QY 51 RDLCTYGTGICGKILEPAAIFHLKLPALNDHDCGLGFENSTGLKRLADGFEFEVLEFRL 110
D 69 KEICEKNDKENSKEETLAKNKLKPKMEKDCQSGFNQALIKTGAILEYQYLDYLD 128
QY 111 LTFEFGKSYINVDVNEILLTKLGMIDQELNKLTKTHYSPPKDRGLGLGKLVYVHRPA 170
D 129 LQNEFGNQEYMEQLSSIRTLQTLKEKINGLITTT---PATNDWLEKMOSSNEWYAN 184
QY 171 FAFYVLAMERKFAQAVRL 191
D 185 AKVILLRSLENFLQFSIRAI 205
DB
RESULT 11
ID IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-94041419; Pubmed-8225400;
RA Andrews A.E., Barchan G.J., Ashmen K., Meusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RT "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA."
RT Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ibrahim B.;
RL Submitted (Oct-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

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CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X62501; CAA44363.1; -
CC EMBL: X68723; CAA48662.1; -
CC EMBL: A19159; CAA01443.1; -
CC PIR: S29549; S29549.
CC HSSP: P05231; 21L6.
CC InterPro: IPR001716; -
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PRO0433; IL6CSF6GF.
CC PRINTS: PRO0434; INTERLEUKIN6.
CC PROSITE: PS00254; INTERLEUKIN6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT CHAIN 1 29 BY SIMILARITY.
FT DISULEPT 30 208 INTERLEUKIN-6.
FT DISULEPT 72 78 BY SIMILARITY.
FT CARBOHYD 101 111 BY SIMILARITY.
FT CONFLICT 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC966C13E3320A0 CMC64;

Query Match 13.7%; Score 150; DB 1; Length 208;
Best Local Similarity 26.2%; Pred. No. 2.5e-07;
Matches 37; Conservative 30; Mismatches 70; Indels 4; Gaps 1;

OY 51 RDLCTRTGICKGILEPAIPIHLKIPAINIDHICGLIGNENSKKLADGFEFEVLFKR 110
DB 69 KEIEKNDCEENSKETILAENKILPMERKDCFGSGFNQAICTKTAGLETQITLDF 128
OY 111 LTFEPGKSVINVDWELLITWLGMDIQEELNKLRTYHSPPKDFGLGLQGLKVVRR 170
DB 129 LQNEFEGNOEVEWELQSIITLIQIKERIAQLITTT----PATHTDMLKKQSSNEWVKN 184
OY 171 FASRYVLAMKFAAGAVYL 191
DB 185 AKVILIRSLLENLPISIRAI 205

RESULT 12
IL6_MOUSE STANDARD; PRT; 211 AA.
ID IL6_MOUSE
AC P08505;
DT 01-AUG-1988 (Ref. 08, Created)
DT 01-AUG-1988 (Ref. 08, Last sequence update)
DT 15-JUL-1998 (Ref. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (INTERLEUKIN HP-1) (B-CELL HYBRIDOMA
DE GROWTH FACTOR).
GN IL6 OR IL-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE=8816883; PubMed=2965020;
RA van Snick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,
RA Boon T., Simpson R.J.;
RA *cDNA cloning of murine Interleukin-HP1: homology with human
RA Interleukin 6";
RA Eur. J. Immunol. 18:193-197(1988).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=89035525; PubMed=3263439;
RA Tanabe O., Akita S., Kamaya T., Wong G.C., Hirano T., Kishimoto T.;
RT "Genomic structure of the murine IL-6 gene. High degree conservation
RT of potential regulatory sequences between mouse and human.";
RN J. Immunol. 141:3875-3881(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BA16/C;
RX MEDLINE=91057159; PubMed=2243807;
RA Grenett H.E., Fuentes N.L., Fuller G.M.;
RT "Cloning and sequence analysis of the cDNA for murine Interleukin-6.";
RN Nucleic Acids Res. 18:6455-6455(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89017145; PubMed=3262872;
RA Chiu C.P., Moulds C., Coffman R.L., Rennick D., Lee F.;
RT "Multiple biological activities are expressed by a mouse Interleukin
RT 6 cDNA clone isolated from bone marrow stromal cells.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).
RN [5]
RP SEQUENCE OF 5-211 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=89124383; PubMed=2563387;
RA Mock B.A., Nordan R.P., Justice M.J., Kozak C., Jenkins N.A.,
RA Copeland N.G., Clark S.C., Wong G.G., Rudikoff S.;
RT "The murine IL-6 gene maps to the proximal region of chromosome 5.";
RN J. Immunol. 142:1372-1376(1989).
RN [6]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=BA16/C;
RX MEDLINE=90171860; PubMed=2106569;
RA Blankenstein T., Qin Z., Li W., Diamantstein T.;
RT "DNA rearrangement and constitutive expression of the Interleukin 6
RT gene in a mouse plasmacytoma.";
RN J. Exp. Med. 171:965-970(1990).
RN [7]
RP SEQUENCE OF 25-211.
RX MEDLINE=8832059; PubMed=3262059;
RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
RT sequence and relation to human Interleukin-6.";
RN Eur. J. Biochem. 176:187-197(1988).
RN [8]
RP SEQUENCE OF 66-75; 78-84 AND 128-148.
RX MEDLINE=90147691; PubMed=2302197;
RA Jahnke W., Hard L.D., Reid G.E., Moritz R.L., Simpson R.J.;
RT "Internal amino acid sequencing of proteins by in situ cyanogen
RT bromide cleavage in polyacrylamide gels.";
RN Biochem. Biophys. Res. Commun. 166:139-145(1990).
RN [9]
RP SEQUENCE OF 25-45.
RX MEDLINE=87092311; PubMed=2948184;
RA van Snick J., Cayphas S., Vink A., Uytendhoe C., Coulle P.G.,
RA Rudira M.R., Simpson R.J.;
RT "Purification and NH2-terminal amino acid sequence of a
RT T-cell-derived lymphokine with growth factor activity for B-cell
RT hybridomas.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
RN [10]
RP -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
RP FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
RP OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
RP PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
RP HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
RN [11]
RP -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
RN [12]

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DR EMBL: X57317; CAA40572.1; -
 DR PIR: S22162; S22162.
 DR HSSP: P05231; 21L6.
 DR InterPro: IPR001716; -
 DR Pfam: PF004489; IL6; 1.
 DR PRINTS: PRO0433; IL6GSPMGF.
 DR PROSITE: PRO0434; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE: Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 208
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 38 38
 FT SEQUENCE 208 AA; 23758 MW; A0F00DB9BA2EC341 CRC64; (POTENTIAL).

Query Match 13.1%; Score 143.5; DB 1; Length 208;
 Best Local Similarity 24.4%; Pred. No. 1e-06;
 Matches 42; Conservative 37; Mismatches 86; Indels 7; Gaps 2;

QY 20 TRGKLPDAPPEERDLIQRNLNMLWYIDECFRLDRCRGICGILEPRAITHLTPAIND 79
 DB 41 TPGRLLTPKTKALIKR--WVDKISAMRKICRKNDECSSEYLAENKLNPKME 97
 QY 80 TDHCGILGFNETSCLKRLADGFEFEVLFKFLTEGKSVINVDWELLTTLGMDIOE 139
 DB 98 KDCGFOSGFNOALICLTITTAGLEIYDIYQNEEGQENVNDRLRNITLQILKOK 157
 QY 140 LNKLTFRHYSPKFRCLGLRGLKLVYVHRFASFYVLSAMEKFAQAVRVL 191
 DB 158 IADLTIT---PATNTDLKMQSSNENYKNAKIILLNLENFLQESLRAI 205

RESULT 15
 IL6_MARMO STANDARD; PRT; 207 AA.
 AC O35736;
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last sequence update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OC NCBI_Taxid=9995;
 RX MEDLINE=98139533; Pubmed=9472070;
 RX Lohrengel B., Lu M., Roggendorf M.;
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
 and IL-6."
 RL Immunogenetics 47:332-335(1998).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: Y14139; CAA74571.1; -
 DR InterPro: IPR001716; -
 DR Pfam: PF004489; IL6; 1.
 DR PRINTS: PRO0433; IL6GSPMGF.
 DR PRINTS: PRO0434; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE: Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 207
 FT DISULFID 65 71
 FT DISULFID 94 104
 FT SEQUENCE 207 AA; 23770 MW; F30D19F86DA6A00 CRC64; (POTENTIAL).

Query Match 12.3%; Score 135; DB 1; Length 207;
 Best Local Similarity 22.6%; Pred. No. 6.7e-06;
 Matches 47; Conservative 42; Mismatches 93; Indels 26; Gaps 6;

QY 5 KLSILLVGSLLV-----SGTRGKLPDAPPEERDLIQRNLNMLWYID 47
 DB 2 KFFSIASIGLLLVATAFPASELQREDEGSESVTRNK-PTASSGKTR--RQISYLIVEVF 58
 QY 48 ECFRDLICRGICGILEPRAIF--HLKLPAINDDHCLGIFNETSCLKRLADGFEFE 105
 DB 59 EMKRELCANDETC--IKSHVAVSENNINLPKMKRQCCQYOTYNNDDLVNITSGLEFP 116
 QY 106 VLFKFLTEF--GKSVINVDWELLTKTLQMDIOEILNLTTHNSPPKFRCLGLRLOG 163
 DB 117 VYLRIYRNKFEQGNRRRAEHVQSSKALIEILKQVKDPNKIVPPPTANINILAKLES 176
 QY 164 LKMYVHRFASFYVLSAMEKFAQAVRVL 191
 DB 177 QNDMKVATMQLIISNFDPLQFTLRVAV 204

Search completed: October 4, 2001, 19:12:31
 Job time: 266 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:08 ; Search time 54.44 Seconds
(without alignments)
21.158 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105

Perfect score: 103

Sequence: 1 GFNETSCLKMLADGFFEEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/AA1981.DAT:*
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6: /SIDSI/gcgdata/geneseq/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/AA1989.DAT:*
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16: /SIDSI/gcgdata/geneseq/AA1995.DAT:*
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18: /SIDSI/gcgdata/geneseq/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	103	100.0	19	AAW23945	Human herpesvirus
2	103	100.0	185	AAW5015	Kaposi's sarcoma h
3	103	100.0	204	AAW74570	Kaposi sarcoma her
4	103	100.0	204	AAW40103	Human herpesvirus
5	103	100.0	204	AAW23944	Human herpesvirus
6	61	59.2	162	AAW7391	Human mutant IL-6a
7	61	59.2	162	AAW00131	Human interleukin-
8	61	59.2	163	AAW00132	Human interleukin-
9	61	59.2	167	AAW77649	Human interleukin-
10	61	59.2	169	AAW7387	Human IL-6 mutant
11	61	59.2	174	AAW5342	Hybrid human cyto

12	61	59.2	176	AAW5341	Hybrid human cyto
13	61	59.2	177	AAW7398	Human IL-6 mutant
14	61	59.2	179	AAW7334	Human interleukin-
15	61	59.2	183	AAW60125	Human interleukin
16	61	59.2	184	AAW81158	Polypeptide with B
17	61	59.2	184	AAW94753	Sequence of varian
18	61	59.2	184	AAW6532	Human B-cell stimu
19	61	59.2	184	AAW03914	Human B-cell stimu
20	61	59.2	184	AAW02793	Polypeptide with h
21	61	59.2	184	AAW72219	Interleukin-6. A
22	61	59.2	184	AAW54930	Human Interleukin-
23	61	59.2	184	AAW55256	Mutant Interleukin
24	61	59.2	184	AAW74659	Interleukin 6. Ho
25	61	59.2	184	AAW68623	Interleukin-6 for
26	61	59.2	184	AAW07199	B-cell differentia
27	61	59.2	184	AAW07200	Human Interleukin
28	61	59.2	184	AAW07201	Human Interleukin
29	61	59.2	184	AAW07197	Human Interleukin
30	61	59.2	184	AAW07198	Human Interleukin
31	61	59.2	184	AAW02609	Interleukin-6. Ho
32	61	59.2	184	AAW02610	Interleukin-6. Ho
33	61	59.2	184	AAW02611	Interleukin-6 (F74
34	61	59.2	184	AAW02612	Interleukin-6 (Q75
35	61	59.2	184	AAW08476	Interleukin-6 vari
36	61	59.2	184	AAW08477	Interleukin-6 vari
37	61	59.2	184	AAW08478	Interleukin-6 vari
38	61	59.2	184	AAW58518	Human Interleukin
39	61	59.2	184	AAW58519	Human Interleukin
40	61	59.2	184	AAW92803	Human IL-16 mutcin
41	61	59.2	185	AAW81159	Polypeptide with B
42	61	59.2	185	AAW90059	Human Ala B cell d
43	61	59.2	185	AAW94754	Sequence of varian
44	61	59.2	185	AAW91015	Synthetic interlev
45	61	59.2	185	AAW05275	Segment of human B

ALIGNMENTS

RESULT	ID	AAW23945	standard. Protein. 19 AA.
AC	AAW23945;		
XX			
DT	01-JUL-1998	(first entry)	
XX			
DE	Human herpesvirus 8	Interleukin-6 fragment.	
XX			
KW	Interleukin-6: IL-6: human herpesvirus 8; HHV8;		
KM	shotgun-cloning; Antibodies; diagnosis; treatment.		
OS	Human herpesvirus 8.		
XX			
PN	W09803657-A1.		
XX			
PD	29-JAN-1998.		
XX			
PF	19-JUL-1996.	96WO-EP03199.	
XX			
PR	19-JUL-1996.	96WO-EP03199.	
XX			
PA	(BEHW) BEHRING DIAGNOSTICS GMBH.		
PA	(UWNY) UNIV NEW YORK STATE.		
XX			
PI	Albrecht J, Fleckenstein B, Friedman-kien A, Huang Y;		
PI	Neipel F.		
DR	WPI; 1998-120781/11.		
XX			
PT	Viral Interleukin-6 produced recombinantly from human herpes virus 8		
PT	DNA - and related nucleic acid and antibodies, used for diagnosis		
PT	and treatment of herpes 8 infection or related diseases, e.g. Kaposi		

PT sarcoma
XX
PS Claim 4; Page 8; 19pp: English.
CC The interleukin-6 (IL-6) fragment and protein AAW23944 can be used to
CC detect antibodies and antibodies can be used to detect IL-6. This can
CC be used for the diagnosis of HIV8 infection or associated diseases such
CC as Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the
CC gene sequence can all be used in the treatment of infections and
CC diseases as mentioned above.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 103; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 2, 6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GENETSCIKTADCPFEFE 19
Db | |||||
1 gfnetsciklndgltfete 19

RESULT 2
ID AAM95015 standard; peptide: 185 AA.
AC AAM95015;
DE 21-MAY-1999 (first entry)
XX Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
XX Cytokine: Interleukin-B30; IL-B30; forensic science; cell proliferation;
XX Inflammatory condition; drug screening; human; IL-6.
XX Kaposi's sarcoma herpes virus.
XX MO905280-A1.
PN 04-FEB-1999.
PD 24-JUL-1998; 98MO-US15423.
XX 25-JUL-1997; 97US-0900905.
PR (SCHE) SCHERING CORP.
XX Bazan JF;
XX MPI; 1999-142935/12.
DR NEWLY isolated or recombinant polynucleotide encoding mammalian
PT Interleukin-B30 (IL-B30), including fragments - useful for
PT regulating activation, development, differentiation and function of
PT various cell types, and for diagnosing and treating conditions
PT associated with IL-B30
PS Disclosure: Page 11-12; 83pp; English.

This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
polypeptides. Host cells containing a vector comprising the IL-B30
nucleic acids are used for the recombinant production of the proteins.
The polynucleotides are useful for diagnosis of IL-B30 mediated
conditions, and forensic science (e.g. to distinguish rodent from human,
or as a marker to distinguish between different cells exhibiting
differential expression or modification patterns). The IL-B30 (including
fragments), together with antibodies that bind to IL-B30 are useful for
teaching purposes. They are also used for treating conditions associated
with abnormal physiology or development, including inflammatory
conditions. The polypeptide cytokine should mediate cytokine synthesis
and proliferation in cells. IL-B30 is useful for drug screening to
identify compounds having binding affinity to IL-B30. The present

OY 1 GFNETSCLKTLADGFFFE 19
 Db 87 gfnetscLkkladgffefe 105

RESULT 4

AAW40103
 ID AAW40103 standard; Protein: 204 AA.

XX AAW40103;

XX 15-JUL-1998 (first entry)

XX Human herpesvirus 8 (HHV-8) Interleukin-6.

XX DL-B: thymidylate synthase; dihydrofolate reductase; primer: HHV-8;

XX Bcl-2 homologue; IE-1A; IE-1B: viral macrophage inhibitory protein;

XX Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.

XX Kaposi's sarcoma associated herpesvirus.

XX WO9804284-A1.

XX 05-FEB-1998.

XX 24-JUL-1997; 97MO-US12931.

XX 25-JUL-1996; 96US-0022591.

XX (UYXO) UNIV JOHNS HOPKINS.

XX Hardwick JM, Hayward GS, Nicholas J, Reltz MR;

XX WPI; 1998-130422/12.

XX New human herpes virus gene region containing 8 open reading frames

XX large cell lymphoma

XX Claim 1; Pages 59-60; 84pp; English.

XX The sequence represents a novel human herpesvirus 8 (HHV-8)

XX Interleukin-6. The invention claims for novel genes, which includes

XX the viral Interleukin-6 gene, found at the divergent DL-B locus. HHV-8

XX divergent locus DL-B lies between open reading frames 11 and 17.

XX Sequencing of the HHV-8 divergent locus DL-B revealed the presence of

XX nine viral ORFs with gene products related to cellular proteins. These

XX proteins include the thymidylate synthase (TS, AAW40100), dihydrofolate

XX reductase (DHFR, see AAW40101), Bcl-2 homologue (AAW40102), IE-1A

XX Interleukin-6 (vIL-6), viral macrophage inhibitory protein (vMIP)-1A

XX (AAW40104) and -1B (AAW40105) and beta-chemokine-like (BCK, AAW40106)

XX protein. The invention claims the mentioned proteins and a

XX polynucleotide containing HHV-8 genes encoding one or more of these

XX proteins. The invention also claims that the polynucleotide and the

XX proteins may be used directly or indirectly, e.g. using antibodies to the

XX proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's sarcoma,

XX Castleman's disease, multiple myeloma and body cavity based large cell

XX lymphoma (BCHL). The proteins have also been claimed to be useful in

RESULT 5

AAW23944
 ID AAW23944 standard; Protein: 204 AA.

XX AAW23944;

XX 30-JUN-1998 (first entry)

XX Human herpesvirus 8 Interleukin-6.

XX Interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;

XX antibody; diagnosis; treatment.

XX Human herpesvirus 8.

XX WO9803657-A1.

XX 29-JAN-1998.

XX 19-JUL-1996; 96MO-EP03199.

XX 19-JUL-1996; 96MO-EP03199.

XX (BEHW) BEHRING DIAGNOSTICS GMBH.

XX (UYNY) UNIV NEW YORK STATE.

XX Albrecht J, Fleckenstein B, Friedman-kien A, Huang Y;

XX Neipel F;

XX WPI; 1998-120781/11.

XX Viral interleukin-6 produced recombinantly from human herpes virus 8

XX DNA - and related nucleic acid and antibodies, used for diagnosis

XX and treatment of herpes 8 infection or related diseases, e.g. Kaposi

XX Sarcoma

XX Claim 2; Fig 2; 19pp; English.

XX The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence

XX can be used to detect antibodies and antibodies can be used to detect

XX IL-6. This can be used for the diagnosis of HHV8 infection or

XX associated diseases such as Kaposi sarcoma or kidney cell carcinoma.

XX Antibodies, proteins and the gene sequence can all be used in the

XX treatment of infections and diseases as mentioned above.

XX Sequence 204 AA;

XX AAW23944

XX ID AAW23944 standard; Protein: 162 AA.

XX AAW23944;

XX 17-APR-1996 (first entry)

XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).

XX Human Interleukin-6; IL-6a/C1 mutant; increased stability;

XX recombinant; Production; deletion mutant;

XX amino acids 5-19 and 44-50.

XX Homo sapiens.

RESULT 6

AAW77391
 ID AAW77391 standard; Protein: 162 AA.

XX AAW77391;

XX 17-APR-1996 (first entry)

XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).

XX Human Interleukin-6; IL-6a/C1 mutant; increased stability;

XX recombinant; Production; deletion mutant;

XX amino acids 5-19 and 44-50.

XX Homo sapiens.

XX JP07224097-A.
 XX 22-AUG-1995.
 PD 08-FEB-1994; 94JP-0014461.
 XX 08-FEB-1994; 94JP-0014461.
 XX 08-FEB-1994; 94JP-0014461.
 XX (ASAG) ASAH I GLASS CO LTD.
 PA WPI: 1995-325556/42.
 DR N-PSDB: AAQ94346.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural Interleukin-6
 PS Claim 1; Page 14; 18pp; Japanese.
 XX AAQ94346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl,
 CC which lacks the amino acids Gly5-Leu19 and Cys84-Cys80 of the
 CC wild type protein. The cDNA can be used for the recombinant prodn.
 CC of IL-6a'Cl, which has increased stability compared to wild type
 CC IL-6.
 XX Sequence 162 AA;
 SQ

Query Match 59.2%; Score 61; DB 16; Length 162;
 Best Local Similarity 57.9%; Pred. No. 0.018;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKRLADGFEFE 19
 ||||:||||:|
 Db 55 gfnectclvklitglltfe 73

RESULT 7

AAW00131
 ID AAW00131 standard; Protein: 162 AA.

XX AAW00131;
 AC 09-APR-1997 (first entry)
 XX Human Interleukin-6 fragment.

DE Secretary; signal peptide; P-factor; multicloning vector; PCR;
 KW animal protein; expression; production; recombinant; primer;
 KW fission yeast; human; serum albumin; interleukin-6;
 KW polymerase chain reaction; Schizosaccharomyces pombe;
 KM PO fragment.

XX Homo sapiens.

OS WO9623890-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASAH I GLASS CO LTD.

XX Hama Y, Kumagai H, Nikaïdo K, Tohda H, Tsukamoto H;
 PI WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene
 PT - for production of vectors for expression of animal proteins in a
 PT fission yeast, pref. S. pombe, host
 XX

PS Example 4; Pages 28-29; 50pp; Japanese.
 XX A multicloning vector comprising the human interleukin-6 (hIL-6)
 CC cDNA, a Schizosaccharomyces pombe secretory signal peptide
 CC fragment or P-factor fragment (PO fragment) DNA and preferably an
 CC animal cell viral promoter sequence and a neomycin resistance gene,
 CC can be used for the efficient production of a hIL-6 fragment, i.e.,
 CC the present sequence, in a fission yeast host, preferably S. pombe,
 CC culture.
 XX Sequence 162 AA;
 SQ

Query Match 59.2%; Score 61; DB 17; Length 162;
 Best Local Similarity 57.9%; Pred. No. 0.018;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKRLADGFEFE 19
 ||||:||||:|
 Db 55 gfnectclvklitglltfe 73

RESULT 8

AAW00132
 ID AAW00132 standard; Protein: 163 AA.

XX AAW00132;
 AC 09-APR-1997 (first entry)
 XX Human Interleukin-6 fragment.

DE Secretary; signal peptide; P-factor; multicloning vector; PCR;
 KW animal protein; expression; production; recombinant; primer;
 KW fission yeast; human; serum albumin; interleukin-6;
 KW polymerase chain reaction; Schizosaccharomyces pombe;
 KM PI fragment.

XX Homo sapiens.
 OS WO9623890-A1.
 XX 08-AUG-1996.
 XX 01-FEB-1996; 96WO-JP00198.
 XX 03-FEB-1995; 95JP-0017167.
 XX (ASAG) ASAH I GLASS CO LTD.
 XX Hama Y, Kumagai H, Nikaïdo K, Tohda H, Tsukamoto H;
 PI WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene
 PT - for production of vectors for expression of animal proteins in a
 PT fission yeast, pref. S. pombe, host
 XX Example 7; Pages 30-31; 50pp; Japanese.
 XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
 CC cDNA, a Schizosaccharomyces pombe secretory signal peptide
 CC fragment or P-factor fragment (PI fragment) DNA and preferably an
 CC animal cell viral promoter sequence and a neomycin resistance gene,
 CC can be used for the efficient production of a hIL-6 fragment, i.e.,
 CC the present sequence, in a fission yeast host, preferably S. pombe,
 CC culture.
 XX Sequence 163 AA;
 SQ

Query Match 59.2%; Score 61; DB 17; Length 163;
 Best Local Similarity 57.9%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENEISCLKRLADGFFEE 19
 |||| :|| :| |||
 Db 56 gfnecclvklitglltfe 74

RESULT 9

AAR77649
 ID AAR77649 standard; Protein: 167 AA.

AC AAR77649;

DT 27-JUN-1996 (first entry)

DE Human interleukin-6 splice variant.

XX Human; interleukin-6; splice variant; IL-6SV; treatment;

KW immunotherapy; anti-inflammatory; bone marrow transplant;

KW chemotherapy; side effect; corneal damage; keratitis; ulcer;

KW antagonist; Castleman's disease; multiple myeloma;

KW cardiac myxoma; cervical cancer; rheumatoid arthritis;

KW autoimmune diabetes; sepsis.

OS Homo sapiens.

XX WO9532282-A1.

PN 30-NOV-1995.

PD 17-MAY-1995; 95WO-US06094.

PF 19-MAY-1994; 94US-0246427.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Li H, Ruben S;

PI WPI; 1996-020577/02.

DR N-PSDB; AAT08558.

XX Polynucleotide encoding Interleukin 6-splice variant - used for

PT treating auto-immune diseases and inflammation.

XX Claim 1; Page 40; 54pp; English.

PS The human interleukin-6 splice variant (IL-6SV) AAR77649 is encoded

CC by AAT08558 (which is derived from an activated macrophage cDNA

CC library) and may be used in immunotherapeutic and

CC anti-inflammatory compounds, and for the treatment of patients

CC suffering from bone marrow transplant chemotherapy side effects,

CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may

CC be used to treat diseases caused by the up-regulated prodn. of

CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,

CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),

CC and sepsis.

XX SQ Sequence 167 AA;

Query Match 59.2%; Score 61; DB 17; Length 167;

Best Local Similarity 57.9%; Pred. No. 0.019;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENEISCLKRLADGFFEE 19
 |||| :|| :| |||
 Db 60 gfnecclvklitglltfe 78

RESULT 10

AAR77387
 ID AAR77387 standard; Protein: 169 AA.

AC AAR77387;

XX 17-APR-1996 (first entry)

DT Human IL-6 mutant IL-6a (amino acids 5-19 deleted).

XX Human interleukin-6; IL-6a mutant; increased stability;

KW recombinant; production; deletion mutant; amino acids 5-19.

OS Homo sapiens.

XX JP07224097-A.

PN 22-AUG-1995.

PD 08-FEB-1994; 94JP-0014461.

PF 08-FEB-1994; 94JP-0014461.

PR (ASAG) ASahi GLASS CO LTD.

XX WPI; 1995-325556/42.

DR N-PSDB; AAQ94342.

XX Interleukin-6 mutant, related DNA and expression vectors - has

PT higher stability than natural Interleukin-6

XX Claim 1; Page 10; 18pp; Japanese.

PS AAQ94342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which

CC lacks the amino acids Gly5-Ileu19 of the wild type protein. The

CC cDNA can be used for the recombinant prodn. of IL-6a, which has

CC increased stability compared to wild type IL-6.

XX SQ Sequence 169 AA;

Query Match 59.2%; Score 61; DB 16; Length 169;

Best Local Similarity 57.9%; Pred. No. 0.019;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENEISCLKRLADGFFEE 19
 |||| :|| :| |||
 Db 62 gfnecclvklitglltfe 80

RESULT 11

AAR75342
 ID AAR75342 standard; Protein: 174 AA.

AC AAR75342;

XX 13-DEC-1995 (first entry)

DT Hybrid human cytokine IIII.

XX Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 173

XX MISC-difference 173

XX WO9513393-A.

PN 18-MAY-1995.

PD 07-NOV-1994; 94WO-US12873.

PF 08-NOV-1993; 93US-0149101.

PR (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

[illegible]

DR WP1: 1995-194111/25.
DR N-PSDB: AA087160.

PT New hybrid cytokines with alpha helical sequences from different
PT sources - also DNA encoding them, vectors and transformed cells,
PT useful e.g. for treating cancer, remodelling bone etc.

PS Claim 11; Page 30; 52pp; English.

CC The cytokine encoding genes for leukemia inhibitory factor (IL),
CC granulocyte-colony stimulating factor (G), interleukin-6 (IL),
CC interleukin-11 (E), ciliary neurotrophic factor (C) and
CC interferon-gamma (I) have been cloned and reported in the literature.
CC I, G, L, E, C and O each comprise four alpha-helical sequences. In
CC alpha-helical 'linking' sequences of about 5-100 AAs. The invention
CC provides a group of therapeutic hybrid cytokines, having a size ranging
CC from about 10 to about 30 kDa. Each hybrid cytokine comprises three or
CC four alpha-helical sequences and linking sequences, ranging from about
CC 5-40 AAs in length. In the nomenclature of the hybrid cytokines,
CC upper case letters designate alpha-helical sequences, lower case
CC letters (whether Arabic numerals, alphabetic or symbolic) indicate
CC a specific linking sequence. The first three alpha-helical
CC sequences of IL1L and IL1L-alpha were derived from IL-6 and the
CC fourth alpha-sequence was derived from LIF. IL1L-alpha has two
CC additional AAs inserted in a linking sequence between alpha-helices
CC III and IV, as compared with IL1L.

SX Sequence 176 AA;

OY Query Match 59.2%; Score 61; DB 16; Length 176;
Best Local Similarity 57.9%; Pred. NO. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0.

Db 1 GENESOLKRLADGFEEF 19
|||:|||:|||||
78 glnetctvkvkltglllefe 96

RESULT 13
AAR77388
ID AAR77388 standard; Protein; 177 AA.
XX AAR77388:
AC
DT 17-APR-1996 (first entry)
XX
XX Human IL-6 mutant IL-6C1 (amino acids 44-50 deleted).
DE
XX
XX Human interleukin-6; IL-6C1 mutant; increased stability;
KW recombinant; production; deletion mutant; amino acids 44-50.
XX
XX Homo sapiens.
OS
PN JP07224097-A.
XX
XX 22-AUG-1995.
PD
XX
XX 08-FEB-1994; 94JP-0014461.
PE
XX
XX 08-FEB-1994; 94JP-0014461.
PR
XX
XX (ASAG) ASAMI GLASS CO LTD.
PA
XX
XX WP1: 1995-325556/42.
DR
DR N-PSDB: AAQ94343.
XX
XX Interleukin-6 mutant, related DNA and expression vectors - has
XX higher stability than natural Interleukin-6
XX
XX Claim 1; Page 11; 18pp; Japanese.

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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:51 ; Search time 44.98 Seconds
(Without alignments)
32.177 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105

Perfect score: 103
Sequence: 1 GFNETSCLKKLADGFFPEFE 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	59.2	212	1	IVHUB2
2	55	53.4	208	2	interleukin-6 prec
3	53	51.5	212	2	T09216
4	53	51.5	212	2	I46621
5	51	49.5	207	2	I46590
6	49	47.6	211	2	I46084
7	48	46.5	162	2	A34247
8	47	45.6	211	1	HR3786
9	47	45.6	211	1	ICMS5
10	46	44.7	208	1	T05375
11	46	44.7	208	1	S29349
12	45	43.7	484	2	C82379
13	44	42.7	282	2	F71061
14	44	42.7	282	2	D70149
15	44	42.7	1893	2	T27249
16	44	42.7	1893	2	T22661
17	44	42.7	2875	1	RRVUTW
18	44	42.7	157	2	T43274
19	43	41.7	208	1	H69203
20	43	41.7	231	2	A56610
21	42.5	41.3	492	2	H83664
22	42	40.8	180	2	T30066
23	42	40.8	364	2	H72402
24	42	40.8	512	2	T23819
25	42	40.8	861	2	S47900
26	42	40.8	1690	2	T41945
27	42	40.8	2048	1	T13030
28	42	40.8	2139	2	T13030
29	42	40.8	2228	1	S46404
30	42	40.8	2228	1	ZLNZSV

30	42	40.8	2233	1	ZLNZSV	genome polypeptide
31	41.5	40.3	386	2	B1443	hypothetical prote
32	41	39.8	158	2	T17748	hypothetical prote
33	41	39.8	159	1	E71208	hypothetical prote
34	41	39.8	320	2	S22615	hypothetical prote
35	41	39.8	343	2	JM0249	vancomycin resist
36	41	39.8	669	2	T51220	hypothetical prote
37	41	39.8	787	2	T00798	hypothetical prote
38	41	39.8	1224	2	S25952	gene cod intron 3
39	41	39.8	1642	2	T08880	NMDA receptor-bind
40	40.5	39.3	244	2	U52425	glutathione transf
41	40.5	39.3	695	2	T28782	probable phytocho
42	40.5	39.3	1276	2	S75801	major allergen lo1
43	40	38.8	88	2	A48595	pollen allergen lo
44	40	38.8	97	2	A34291	hypothetical prote
45	40	38.8	152	2	B64485	hypothetical prote

ALIGNMENTS

RESULT 1
IVHUB2
interleukin-6 precursor [validated] - human
N:Interleukin-6 precursor [validated] - human
on factor
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence-revision 28-Dec-1987 #text-change 08-Dec-2000
C:Accession: A32648; A25692; A3515; A25801; A5921; I52193; I56003; A27601;
R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A:Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A:Reference number: A32648; MUID:88082654
A:Accession: A32648
A:Molecule type: DNA
A:Residues: 1-212 <21L>
A:Cross-references: GB:X04430; NID:932673; PIDN:CAA68278.1; PID:932674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwa
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A:Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A:Reference number: A32648; MUID:87053818
A:Accession: A25692
A:Molecule type: mRNA
A:Residues: 1-212 <21L>
A:Cross-references: GB:X04430; NID:932673; PIDN:CAA68278.1; PID:932674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwa
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A:Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A:Reference number: A32648; MUID:87053818
A:Accession: A25692
A:Molecule type: mRNA
A:Residues: 1-212 <21L>
A:Cross-references: GB:X04430; NID:932673; PIDN:CAA68278.1; PID:932674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwa
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A:Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A:Reference number: A32648; MUID:87053818
A:Accession: A3515
A:Molecule type: mRNA
A:Residues: 1-212 <21L>
A:Cross-references: GB:M29150; NID:9186349; PIDN:CAA59154.1; PID:9307063
R:Haegeman, G.; Content, J.; Voickeart, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A:Reference number: A25801; MUID:87004683
A:Accession: A25801
A:Molecule type: DNA; mRNA
A:Residues: 1-212 <21L>
A:Cross-references: GB:X04403
A:Experimental source: fibroblast
R:May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GENETSCLKKLADGFFFE 19
 |||:||||:|
 Db 102 GFNOETCLMRITGGLVERO 120

RESULT 3
 146621
 prointerleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146621
 R:Richards, C.; Saklatva, J.
 Cytokine 3, 269-276, 1991
 A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
 A:Reference number: 146621; MUID:91338547
 A:Accession: 146621
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <RUC>
 A:Cross-references: GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625
 C:Genetics:
 A:Gene: IL6
 C:Superfamily: Interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
 Best Local Similarity 42.1%; Pred. No. 0.33;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GENETSCLKKLADGFFFE 19
 |||:||||:|
 Db 105 GFNOETCLMRITGGLVERO 123

RESULT 4
 146590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146590
 R:Mathalagan, N.; Birdy, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A:Title: Expression of Interleukin-6 in porcine, ovine, and bovine preimplantation conce
 A:Reference number: 146590; MUID:92360284
 A:Accession: 146590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAU>
 A:Cross-references: GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
 Best Local Similarity 42.1%; Pred. No. 0.33;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GENETSCLKKLADGFFFE 19
 |||:||||:|
 Db 105 GFNOETCLMRITGGLVERO 123

RESULT 5
 146084
 Interleukin 6 - cat
 C:Species: Felis silvestris catus (domestic cat)
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
 C:Accession: 146084
 R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
 Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993

A:Title: Molecular cloning and characterization of a cDNA encoding feline Interleukin
 A:Reference number: 146084; MUID:94052249
 A:Accession: 146084
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-207 <BRA>
 A:Cross-references: GB:L16914; NID:g438519; PIDN:AAA16520.1; PID:g438520
 C:Superfamily: Interleukin-6

Query Match 49.5%; Score 51; DB 2; Length 207;
 Best Local Similarity 42.1%; Pred. No. 0.69;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GENETSCLKKLADGFFFE 19
 |||:||||:|
 Db 101 GFNOETCLMRITGGLVERO 119

RESULT 6
 A34247
 Interleukin-6 precursor - rat
 N:Alternate names: IL-6
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
 C:Accession: A34247
 R:Northmann, W.; Bracklak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
 J. Biol. Chem. 264, 16072-16082, 1989
 A:Title: Structure of the rat Interleukin 6 gene and its expression in macrophage-der
 A:Reference number: A34247; MUID:89380206
 A:Accession: A34247
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-211 <NOP>
 A:Cross-references: GB:M26744; NID:g204915; PIDN:AAA17659.1; PID:g204916
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 47.6%; Score 49; DB 2; Length 211;
 Best Local Similarity 44.4%; Pred. No. 1.5;
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 GENETSCLKKLADGFFFE 18
 |||:||||:|
 Db 103 GFNOETCLMRITGGLVERO 120

RESULT 7
 H83786
 hypothetical protein BH1096 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: H83786
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: H83786; MUID:20263314
 A:Accession: H83786
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-162 <STO>
 A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA04815.1; GSPDB:G
 C:Experimental source: strain C-125
 A:Gene: BH1096

Query Match 46.6%; Score 48; DB 2; Length 162;
 Best Local Similarity 66.7%; Pred. No. 1.7;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 TSCIKKLADGFFFE 19

```

DB      31 TSMLEIGADGFFEE 45
|||||
RESULT  8
ICM56
Interleukin-6 precursor - mouse
N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyt
acytoma growth factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
A:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
R:Ratnabe, O.; Akira, S.; Kamita, T.; Wong, G.C.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
A:Reference number: A30531; MIMD:89035525
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <FAN>
A:Cross-references: GB:X0572; NID:q198369; PIDN:AA39302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Sim
Eur. J. Immunol. 18, 193-197, 1988
A:Title: cDNA cloning of murine interleukin-6: homology with human interleukin 6.
A:Reference number: A27610; MIMD:8816883
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-references: GB:X06203; NID:q52701; PIDN:CA29560.1; PID:g52702
R:Mock, B.A.; Jordan, R.P.; Umette, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Clu
J. Immunol. 142, 1372-1376, 1989
A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MIMD:89124383
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOC>
A:Cross-references: GB:A24221; NID:q341131; PIDN:AA68814.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and p
A:Reference number: S01323; MIMD:88329059
A:Accession: S01323
A:Molecule type: protein
A:Residues: 25-166, 'X', 168-211 <SIM>
A:Note: The sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MIMD:91057159
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <GRE>
A:Cross-references: EMBL:X54542; NID:q52727; PIDN:CA34411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A30157; MIMD:90147691
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69, 'X', 71-75, 78-94, 128-148 <JAS>
R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoe, C.; Coulle, P.G.; Rubira, M.R.; SIMP
Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
A:Reference number: A26662; MIMD:87092311
A:Accession: A26662
A:Molecule type: protein
A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clon
A:Reference number: A40486; MIMD:89017145
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>

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A:Cross-references: GB:X03783; NID:q198367; PIDN:AA39301.1; PID:g389410
R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.
Blood 72, 2070-2073, 1988
A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin
A:Reference number: A60799; MIMD:89062753
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a
A:Reference number: S10241; MIMD:90171860
A:Accession: S10241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:q49738; PIDN:CA35824.1; PID:g581860
R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A:Title: Specific covalent modification of the tryptophan residues in murine interleu
A:Reference number: S38254; MIMD:94039075
A:Accession: S38254
A>Status: preliminary
A:Molecule type: protein
A:Residues: 38-60, 75, 'X', 77-79, 176-203 <ZHA>
C:Genetics:
A:Gene: IL-6
A:Map position: 5
A:Insertions: 7/1; 68/3; 156/3
A:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine
F:1-34/Domain: signal sequence #status predicted <SIG>
F:25-211/Product: Interleukin-6 #status experimental <ANT>

```

```

Query Match      45 68; Score 47; DB 1; Length 211;
Best Local Similarity 38 98; Pred. No. 32;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 GENETSCIKLADGFFEE 18
DB      103 GYNORICLKIRISCLLEY 120
|||||
RESULT  9
T05375
Hypothetical protein F16G20.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
A:Accession: T05375
R:Byran, M.; Watson, M.D.; Gibbons, T.; Bartley, J.; Bancroft, I.; Mewes, H.W.; Mayer
submitted to the Protein Sequence Database, August 1998
A:Reference number: 215413
A:Accession: T05375
A:Molecule type: DNA
A:Residues: 1-745 <BEV>
A:Cross-references: EMBL:AL031326
A:Experimental source: cultivar Columbia; BAC clone F16G20
C:Genetics:
A:Map position: 4
A:Insertions: 22/2; 121/1; 159/3; 234/3; 286/3; 366/3; 450/1; 490/3; 519/3; 572/3; 620/3
A:Note: F16G20.70

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Query Match      45 68; Score 47; DB 2; Length 745;
Best Local Similarity 47 18; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 GENETSCIKLADGFFEE 17
DB      289 GPNKTCINTLCPEFTVO 305
|||||

```

RESULT 10
S29549
C:Species: Ovis orientalis arles, Ovis ammon arles (domestic sheep)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S29549
R:Ebrahim, B.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29549
A:Accession: S29549
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <EBR>
A:Cross-references: EMBL:X68723
C:Superfamily: Interleukin-6

Query Match 44.7% Score 46; DB 1; Length 208;
Best Local Similarity 42.1%; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 GFNETSCCKKLADGFEDE 19
||| || | |
DB 105 GFNAVCCLKITWAGLEEQ 123

RESULT 11
S29549
response regulator YCA1086 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
A:Accession: C82379
R:Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gimp, M.L.; Dodson, R.J.;
Chardon, D.; Ermlaeva, M.D.; Yamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanav, J.J.; Venter, J.C.; Fraser, C.M.
Nucleotide 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: C82379
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-568 <HEI>
A:Cross-references: GB:AEO0434; GB:AEO03853; NID:9958531; PID:NAAF96979.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: YCA1086
A:Map position: 2

Query Match 44.7% Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 SCLKKLADGFEDE 18
||| . |||||
DB 460 SSLKETPDGFEFF 472

RESULT 12
F71061
hypothetical protein PH188 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
A:Accession: F71061
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A11000; MUID:98344137
A:Accession: F71061
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-484 <KAN>

```

A:Cross-references: GB:AP000005; NID:93236132; PIDN:BAA30288.1; PID:d1031231; PID:g32
A:Experimental source: strain O73
A>Note: This accession replaces an interim accession for a sequence replaced by Genba
C:Genetics:
A:Gene: PH1188
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1188

Query Match          43.7%; Score 45; DB 2; Length 484;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY      1 GFNETSCLKRIADGFEFL 18
       |:|::|::|::|:
Db       75 GYGKTSIMRALAGIYDY 92

RESULT 13
D70149
Hypothetical protein B0397 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
A:Accession: D70149
R:Frazier, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wilson, D.; Peterson, J.; Kellavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vukobratovic, B.; Bowman, C.; Galand, S.; Fujili, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943
A:Accession: D70149
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1:282 <LEF>
A:Cross-references: GB:AEO01145; GB:AEO00783; NID:92688298; PIDN:AAC66779.1; PID:g2688
A:Experimental source: strain BJ1

Query Match          42.7%; Score 44; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 FNETSCLKRIADGFP 16
       :|:|::|::|:
Db       177 YNNTSGSKRLDSFF 191

RESULT 14
T27249
Hypothetical protein Y5F2A.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T27249
R:Lennard, N.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20331
A:Accession: T27249
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1:454 <MIL>
A:Cross-references: EMBL:AI032641; PIDN:CAA21647.1; GSPDB:GM000022; CBSP:Y5F2A.4
C:Genetics:
A:Gene: CBSP:Y5F2A.4
A:Map position: 4
A:Introns: 17/2; 50/3; 125/3; 159/3; 201/3; 241/2; 353/1; 411/1

Query Match          42.7%; Score 44; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY      3 NETSCLKKLA-----DGPF 16

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Db 177 HETSKKKFAFVCKPCDSYF 196

RESULT 15

T22661
hypothetical protein T01G1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T22661; T24305
R:White, S.; Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19594
A:Accession: T22661
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1893 <M12>
A:Cross-references: EMBL:Z82271; PIDN:CA805214.1; GSPDB:GN00022; CESP:T01G1.1
A:Experimental source: clone F54W12
R:Korshaw, J.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19872
A:Accession: T24305
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1893 <M12>
A:Cross-references: EMBL:Z92811; PIDN:CA807273.1; GSPDB:GN00022; CESP:T01G1.1
A:Experimental source: clone T01G1
C:Genetics:
A:Gene: CESP:T01G1.1
A:Map position: 4
A:Introns: 65/3; 101/3; 194/3; 269/3; 299/2; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1; 9

Query Match 42.7%; Score 44; DB 2; Length 1893;
Best Local Similarity 58.3%; Pred. No. 87;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SCLKKLADGFE 17
||:|||||:
Db 351 SCVEKIVDGLFD 362

Search completed: October 4, 2001, 19:09:53
Job time: 1254 sec


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RL EMBL J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: X04430; CAA28026.1; -
CC DR EMBL: M14584; CAA52728.1; -
CC DR EMBL: X04602; CAA28268.1; -
CC DR EMBL: Y00081; CAA68278.1; -
CC DR EMBL: M18403; CAA52729.1; -
CC DR EMBL: M29150; CAA59154.1; -
CC DR EMBL: X04403; CAA27990.1; -
CC DR EMBL: X04403; CAA27991.1; -
CC DR EMBL: M54894; AAC41704.1; -
CC DR EMBL: S56892; AAD13886.1; -
CC DR EMBL: A09363; CAA00839.1; -
CC DR PIR: A32648; IYH0B2.
CC DR PIR: A25921; A25921.
CC DR PDB: 2116; 04-FEB-98.
CC DR PDB: 2116; 04-FEB-98.
CC DR PDB: 1ALU; 03-JUN-98.
CC DR MIM: 147620; -.
CC DR InterPro: IPR001716; -.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PR00434; IL6GCSFNGF.
CC DR PRINTS: PR00434; INTERLEUKIN_6; 1.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC DR Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78
CC FT CARBOHYD 73 73
CC FT MUTAGEN 173 173 N-LINKED (GLCNAC...).
CC FT MUTAGEN 185 185 A->V: ALMOST NO LOSS OF ACTIVITY.
CC FT MUTAGEN 204 204 W->R: NO LOSS OF ACTIVITY.
CC FT MUTAGEN 210 210 S->P: 13% ACTIVITY.
CC FT MUTAGEN 212 212 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
CC FT MUTAGEN 212 212 M->I,N,S,R: LOSS OF ACTIVITY.
CC SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.0049; Mismatches 6; Indels 0; Gaps 0;
Matches 11; Conservative 2;

QY 1 GENESCKLKLADGFFFE 19
DB 105 GFNEETCLVKITGLLEFE 123

RESULT 3
ID IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9541;
RN (1)
RA SEQUENCE FROM N.A.
RL Tatum M.;
CC Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB000554; BAA19148.1; -
CC DR HSSP: P05231; 2116.
CC DR InterPro: IPR001716; -.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PR00433; IL6GCSFNGF.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC DR Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212 BY SIMILARITY.
CC FT DISULFID 72 78 INTERLEUKIN-6.
CC FT CARBOHYD 73 73 POTENTIAL.
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC...). (POTENTIAL).
CC SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.0049; Mismatches 6; Indels 0; Gaps 0;
Matches 11; Conservative 2;

QY 1 GENESCKLKLADGFFFE 19
DB 105 GFNEETCLVKITGLLEFE 123

RESULT 4
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9544;
RN (1)
RA SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; Pubmed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

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CC EMBL: LA6802; AAB01430.1; -.
DR HSSP: P05231; 21L6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN-6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 209 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
SQ SEQUENCE 209 AA; 23483 MW; 75144922EA3B48E9 CRC64;

Query Match
Best Local Similarity 42.1%; Score 54; DB 1; Length 209;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENESCKKLADGFEFE 19
    |||: |||: | |||:
Db 102 GFNOETCLRTITGLLEFQ 120

RESULT 7
ID IL6_CANFA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Canis familiaris (dog)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MONGREL;
RX MEDLINE=94303924; PubMed=7913298;
RA KUKIELA G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
RA Michael L.H., Ballantyne C.W., Smith C.W., Entman M.L.;
RT *Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion.
RL Ann. N.Y. Acad. Sci. 723:258-270(1994).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: U12234; AAB83030.1; -.
DR HSSP: P05231; 21L6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN-6; 1.
DR PROSITE: PS00254; INTERLEUKIN-6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CONFLICT 30 G -> E (IN REF. 2).
SQ SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match
Best Local Similarity 51.5%; Score 53; DB 1; Length 207;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENESCKKLADGFEFE 19
    |||: |||: | |||:
Db 100 GFNOETCLRTITGLLEFQ 118

RESULT 8
ID IL6_PIG STANDARD; PRT; 212 AA.
AC P26893;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91338547; PubMed=1873476;
RA Richards C., Saklatvala J.;
RT *Molecular cloning and sequence of porcine Interleukin 6 cDNA and
RT expression of mRNA in synovial fibroblasts in vitro.
RL Cytokine 3:269-276(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92360284; PubMed=1497880;
RA Mathalagan N., Bixby J.A., Roberts M.R.;
RT *Expression of Interleukin-6 in porcine, ovine, and bovine
RT preimplantation conceptuses.
RL Mol. Reprod. Dev. 32:324-330(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: M86722; AAC37333.1; -.
DR HSSP: M80258; AAC27127.1; -.
DR HSSP: P05231; 21L6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN-6; 1.
DR PROSITE: PS00254; INTERLEUKIN-6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CONFLICT 30 G -> E (IN REF. 2).
SQ SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match
Best Local Similarity 51.5%; Score 53; DB 1; Length 212;

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IL6_RAT
ID IL6_RAT STANDARD: PRT: 211 AA.
AC P0607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RX SEQUENCE FROM N.A.
MEDLINE=89380206; PubMed=2789217;
Northman W., Brackl T.A., Hattori M., Lee F., Fey G.H.;
Structure of the rat interleukin 6 gene and its expression in
macrophage-derived cells."
RL J. Biol. Chem. 264:16072-16082(1989).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL: M26744; AAA77659.1; -.
DR EMBL: M26745; AAA1430.1; -.
DR PIR: A34247; A34247.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMG.
DR PROSITE: PS00254; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6.
KM Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 47.6%; Score 49; DB 1; Length 211;
Best Local Similarity 44.4%; Pred. No. 0.49;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 GFNETSCLKLIADGFEFF 18
DB 103 GYNDEICLKICGGLLEF 120

RESULT 12
IL6_MARMO
ID IL6_MARMO STANDARD: PRT: 207 AA.
AC O35736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
IL6.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
Marmota.

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OX NCBI_TaxID=9995;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Peripheral blood;
RX MEDLINE=98139533; PubMed=9472070;
RA Lohrangel B., Lu M., Roggendorf M.;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6."
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL: Y14139; CAA74571.1; -.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMG.
DR PROSITE: PS00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6.
KM Cytokine; Growth factor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 207 INTERLEUKIN-6.
FT DISULFID 65 71 POTENTIAL.
FT DISULFID 94 104 POTENTIAL.
SQ SEQUENCE 207 AA; 23770 MW; F30D19F86AD6A600 CRC64;

Query Match 46.6%; Score 48; DB 1; Length 207;
Best Local Similarity 36.8%; Pred. No. 0.7;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 GFNETSCLKLIADGFEFF 19
DB 98 GYNDEICLVIRITGLLEFQ 116

RESULT 13
IL6_MOUSE
ID IL6_MOUSE STANDARD: PRT: 211 AA.
AC P08505;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL HYBRIDOMA
DE GROWTH FACTOR).
IL6 OR IL-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RP MEDLINE=8816883; PubMed=2965020;
RA van Snick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,
RA Boon T., Simpson R.J.;
RT "cDNA cloning of murine interleukin-Hp1: homology with human
RT interleukin 6."
RL Eur. J. Immunol. 18:193-197(1988).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=89035525; PubMed=3263439;
Tanabe O., Akita S., Kamiya T., Wong G.G., Hirano T., Kishimoto T.;

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FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 208 AA: 23423 MW: E92E08BF3E3230A0 CRC64:

Query Match 44.7% Score 46; DB 1; Length 208;
Best local Similarity 42.1%; Pred. No. 1.5;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 GNETSCLKRLADGFEFE 19
DB 105 GFNOAICLIKTTAGLEVO 123

RESULT 15
IL6_SHEEP STANDARD: PRT: 208 AA.
AC P29453;
DT 01-APR-1993 (rel. 25, Created)
DT 01-JUN-1994 (rel. 29, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E., Barclay G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RT "Molecular cloning and characterization of a ruminant Interleukin-6
RT cDNA."
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ebrahim B.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: X62501; CAA44363.1; -;
DR EMBL: X68723; CAA48662.1; -;
DR EMBL: A19159; CAA01443.1; -;
DR PIR: S29549; S29549.
DR HSSP: P05231; 2116.
DR InterPro: IPR001716; -;
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6CSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA: 23446 MW: EEC996C13E3230A0 CRC64:

Query Match 44.7% Score 46; DB 1; Length 208;
Best local Similarity 42.1%; Pred. No. 1.5;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 GNETSCLKRLADGFEFE 19
DB 105 GFNOAICLIKTTAGLEVO 123

Search completed: October 4, 2001, 19:12:32
Job time: 267 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:11:56 ; Search time 74.43 Seconds
(without alignments)
33.774 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105

Perfect score: 103
Sequence: 1 GFNETSCLKKLADGFFFEF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 segs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp_unclassified:*
13: sp-vertebrate:*
14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	204	14	040918
2	103	100.0	204	14	Q98823
3	62	60.2	160	6	Q97535
4	62	60.2	175	6	Q97540
5	61	59.2	209	6	Q97540
6	51	59.2	209	6	Q97540
7	51	59.2	209	6	Q97540
8	51	59.2	209	6	Q97540
9	49	47.6	207	11	Q9JH83
10	49	47.6	207	11	Q9JH83
11	47	45.6	162	2	Q9KDW5
12	46	44.7	568	2	Q9KDW5
13	45	44.2	492	2	Q9KDW5
14	45	43.7	148	7	Q9KDW5
15	45	43.7	207	6	Q28403
16	45	43.7	484	1	Q58908
17	44	42.7	204	10	Q9FK11
18	44	42.7	282	2	051358
19					

20	44	42.7	454	5	Q9XW10	Q9XW10 caenorhabdi
21	44	42.7	1609	5	Q9GRG3	Q9GRG3 caenorhabdi
22	44	42.7	1893	5	Q17887	Q17887 caenorhabdi
23	43	41.7	157	1	Q26871	Q26871 methanobact
24	43	41.7	231	2	Q9KGB5	Q9KGB5 bacillus ha
25	43	41.7	763	2	Q9E2B6	Q9E2B6 zymomonas m
26	43	41.7	1714	10	Q9FPM3	Q9FPM3 arabidopsis
27	42.5	41.3	492	5	Q27470	Q27470 caenorhabdi
28	42	40.8	180	2	Q9W80	Q9W80 thermotoga
29	42	40.8	219	5	Q16639	Q16639 caenorhabdi
30	42	40.8	309	11	Q08763	Q08763 rattus norv
31	42	40.8	364	5	Q21590	Q21590 caenorhabdi
32	42	40.8	460	4	Q95523	Q95523 homo sapien
33	42	40.8	481	4	Q9Y3J7	Q9Y3J7 homo sapien
34	42	40.8	609	4	Q9NZN7	Q9NZN7 homo sapien
35	42	40.8	753	4	Q75175	Q75175 homo sapien
36	42	40.8	948	5	Q9V9G5	Q9V9G5 drosophila
37	42	40.8	1573	11	Q9QX12	Q9QX12 mus musculu
38	42	40.8	1690	5	Q49Z29	Q49Z29 drosophila
39	42	40.8	1690	5	Q9VJ55	Q9VJ55 drosophila
40	42	40.8	1980	14	Q84185	Q84185 human parat
41	42	40.8	2223	14	Q9WFZ5	Q9WFZ5 sendai viru
42	42	40.8	2228	14	Q98705	Q98705 sendai viru
43	42	40.8	2258	14	Q81081	Q81081 human parat
44	42	40.8	2258	14	Q89238	Q89238 human parat
45	41.5	40.3	350	10	Q9FT04	Q9FT04 cicer atle

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	204 AA.
040918	040918			
AC	040918			
DT	01-JAN-1998 (TREMBLrel. 05. Created)			
DT	01-JAN-1998 (TREMBLrel. 05. Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16. Last annotation update)			
DE	ORF K2.			
OS	Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Gammapherpesvirinae; Rhadinovirus.			
OX	NCBI_TaxID=37296;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97138401; PubMed-8985427;			
RA	Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,			
RA	Friedman-Kien A.E., Fleckenstein B.;			
RT	"Human herpesvirus 8 encodes a homolog of Interleukin-6.";			
RL	J. Virol. 71:839-842(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97296220; PubMed-9151804;			
RA	Neipel F., Albrecht J.C., Fleckenstein B.;			
RT	"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus			
RL	human herpesvirus 8: determinants of its pathogenicity?";			
DR	J. Virol. 71:4187-4192(1997).			
DR	EMBL: U93872; AAB62676.1; .			
DR	InterPro: IPR003573; .			
DR	InterPro: IPR003574; .			
DR	PIfam: PF00489; IL6; 1.			
DR	ProDom: PD004356; .; 1.			
DR	SMART: SM00126; IL6; 1.			
SO	SEQUENCE 204 AA; 23408 MW; 2P46737828AF20B9 CRC64;			
Query Match	100.0%; Score 103; DB 14; Length 204;			
Best Local Similarity	100.0%; Pred. No. 2.5e-09;			
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GFNETSCLKKLADGFFFEF 19			
DB	87 GFNETSCLKKLADGFFFEF 105			

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RESULT 2
098823 PRELIMINARY; PRT; 204 AA.
ID 098823
AC 098823
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-6 HOMOLOG (FRAGMENT).
GN IL-6.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Kaposi's sarcoma-associated herpesvirus.
OX NCBI_TaxID=37296;
RN 11
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
RA Friedman-Klen A.E., Fleckenstein B.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA Nicholas J., Ruvoletto V.R., Burns W.H., Sandford G., Wan X., Clufo D.,
RA Hendrickson S., Guo H.G., Hayward G.S., Reltz M.S.;
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RA MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RA "Molecular mimicry of human cytokine and cytokine response pathway
RA genes by KSHV.";
RA Science 274:1739-1744(1996).
RN 14
RP SEQUENCE FROM N.A.
RA MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RA "Nucleotide sequence of the Kaposi sarcoma associated herpesvirus
RA (HHV8).";
RA Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN 15
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN 16
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN 17
RP SEQUENCE FROM N.A.
RA Sun R., Lin S.-F., Miller G.;
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN 18
RP SEQUENCE FROM N.A.
RA EMBL: U73655; AAB18244.1;
DR EMBL: U63774; AAB61701.1;
DR EMBL: U75698; AAC57089.1;
DR EMBL: U71365; AAC34937.1;
DR InterPro: IPR003573;
DR Pfam: PF004489; IL6: 1.
DR SMART: SM00126; IL6: 1.
FT NON_TER 204
FT SEQUENCE 204 AA; 23408 MW; 1CA7772A0BDC05EB CRC64;

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Query Match 100.0%; Score 103; DB 14; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNETSCLKTLADGFFPEE 19
 DB 87 GFNETSCLKTLADGFFPEE 105

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RESULT 3
097535 PRELIMINARY; PRT; 160 AA.
ID 097535
AC 097535
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN 11
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RA "Identification, cloning and sequencing of different Interleukin genes
RA in 4 Aotus species.";
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA EMBL: AF014505; AAD01531.1;
DR HSSP: P05231; IL6.
DR InterPro: IPR003573;
DR InterPro: IPR003574;
DR Pfam: PF004489; IL6: 1.
DR PRINTS: PR00433; IL6GSPMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6: 1.
FT NON_TER 1
FT SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

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Query Match 60.2%; Score 62; DB 6; Length 160;
 Best Local Similarity 57.9%; Pred. No. 0.012;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKTLADGFFPEE 19
 DB 105 GFNETSCLKTLADGFFPEE 123

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RESULT 4
097TH4 PRELIMINARY; PRT; 175 AA.
ID 097TH4
AC 097TH4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nigriceps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN 11
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA EMBL: AF097322; AAF21297.1;
DR HSSP: P05231; IL6.
DR InterPro: IPR002069;
DR InterPro: IPR003573;
DR InterPro: IPR003574;
DR Pfam: PF004489; IL6: 1.
DR PRINTS: PR00433; IL6GSPMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6: 1.
FT NON_TER 1
FT SEQUENCE 175 AA; 18855 MW; 07A021338650A46D CRC64;

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SO SEQUENCE 175 AA; 19205 MW; 28CCE574CB99B189 CRC64;

Query Match 60.2%; Score 62; DB 6; Length 175;

Best Local Similarity 57.9%; Pred. No. 0.013;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GENETSCCLKIADGFFERE 19
 ||||:||||:|
 DB 105 GFNETCLWKITITGLLEFE 123

RESULT 5

O97540 097540 PRELIMINARY; PRT; 209 AA.

AC O97540; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

IL-6.

OS Aotus nancymae (Owl monkey).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=37293;

RN [1] SEQUENCE FROM N.A.

RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murrillo L.A.;

RT "Identification, cloning and sequencing of different interleukin genes

in 4 Aotus species."

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF014510; AAD01536.1;

DR HSSP; P05231; IALU.

DR InterPro; IPR003573;

DR InterPro; IPR003574;

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMC.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

FT NON_TER 1

FT NON_TER 209

SO SEQUENCE 209 AA; 23406 MW; EB4F085DD84002DD CRC64;

Query Match 59.2%; Score 61; DB 6; Length 209;

Best Local Similarity 57.9%; Pred. No. 0.023;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GENETSCCLKIADGFFERE 19
 ||||:||||:|
 DB 105 GFNETCLWKITITGLLEFE 123

RESULT 6

O97TH3 097TH3 PRELIMINARY; PRT; 209 AA.

AC O97TH3; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

IL-6.

OS Aotus lemurinus (Northern gray-necked night monkey).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=43147;

RN [1] SEQUENCE FROM N.A.

RA Murrillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,

RT "Aotus lemurinus gene for IL-6."

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF097323; AAF21298.1;

DR HSSP; P05231; IALU

DR InterPro; IPR003573;

DR InterPro; IPR003574;

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMC.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

FT NON_TER 1

FT NON_TER 209

SO SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match 59.2%; Score 61; DB 6; Length 209;

Best Local Similarity 57.9%; Pred. No. 0.023;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GENETSCCLKIADGFFERE 19
 ||||:||||:|
 DB 105 GFNETCLWKITITGLLEFE 123

RESULT 7

O9WTZ7 09WTZ7 PRELIMINARY; PRT; 207 AA.

AC O9WTZ7; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

IL-6.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1] SEQUENCE FROM N.A.

RA Youn H.-Y., Shin I.-S.;

RT "Canine IL-6 mRNA."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF275796; AAF6275.1;

DR InterPro; IPR003573;

DR InterPro; IPR003574;

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMC.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

SO SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

Query Match 51.5%; Score 53; DB 6; Length 207;

Best Local Similarity 42.1%; Pred. No. 0.48;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 GENETSCCLKIADGFFERE 19
 ||||:||||:|
 DB 100 GFNETCLWKITITGLLEFE 118

RESULT 8

O9XT80 09XT80 PRELIMINARY; PRT; 208 AA.

AC O9XT80; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

IL-6.

OS Delphinapterus leucas (Beluga whale).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;

OC Monodontidae; Delphinapterus.

OX NCB1_TaxID=9749;
 RM 111
 RP SEQUENCE FROM N.A.
 RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
 RT "Molecular cloning and phylogenetic analysis of beluga whale
 (Delphinapterus leucas) interleukin 6."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF076643; AAD42929.1;
 DR HSSP: P05231; IALU.
 DR InterPro: IPR003573;
 DR InterPro: IPR003574;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GSEPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6.
 DR SMART: SM00126; IL6; 1.
 SO SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match 49.5%; Score 51; DB 6; Length 208;
 Best Local Similarity 36.8%; Pred. No. 1;
 Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKILADGFEFE 19
 DB 100 GFNETCLMRLITTCLEYO 118

RESULT 9
 ID 09JHH3 PRELIMINARY; PRT: 207 AA.

AC 09JHH3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eulhelia; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 CC Marmota.
 OC NCB1_TaxID=9995;
 OX 111
 RN SEQUENCE FROM N.A.
 RP TISSUE=PERIPHERAL BLOOD;
 RA Li D.H., Gullen J.M.;
 RT "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis."
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR 12)
 RP SEQUENCE FROM N.A.
 RA Li D.H., Gullen J.M.;
 RT "Gene Structure of the Woodchuck Interleukin-6."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF012908; AAF34861.1;
 DR EMBL: AF122896; AAF28873.1;
 DR InterPro: IPR003573;
 DR InterPro: IPR003574;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GSEPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6.
 DR SMART: SM00126; IL6; 1.
 SO SEQUENCE 207 AA; 23645 MW; AD2FA6E450E13470 CRC64;

Query Match 47.6%; Score 49; DB 11; Length 207;
 Best Local Similarity 36.8%; Pred. No. 2.2;
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 GFNETSCLKILADGFEFE 19
 DB 98 GYNKNCVLVRLITSCLEPFO 116

RESULT 10
 ID 09KDN5 PRELIMINARY; PRT: 162 AA.

AC 09KDN5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE BH1096 PROTEIN.
 GN BH1096.
 OS Bacillus halodurans.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 OX NCB1_TaxID=8665;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RA Takami H., Nakasone K., Takaki Y.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP001510; BAB04815.1;
 SO SEQUENCE 162 AA; 19156 MW; F03A098FEA1FAB73 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 162;
 Best Local Similarity 66.7%; Pred. No. 2.5;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 TSCLKILADGFEFE 19
 DB 31 TSMLGADGFEFE 45

RESULT 11
 ID 081733 PRELIMINARY; PRT: 745 AA.

AC 081733;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 83.1 KDA PROTEIN.
 GN F16G20.70 OR A74G23370.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II;
 CC Brassicales; Brassicaceae; Arabidopsis.
 OX NCB1_TaxID=3702;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Watson M.D., Gibbons T., Bartley J., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C., Bevan M.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR 12)
 RP SEQUENCE FROM N.A.
 RA Watson M.D., Gibbons T., Bartley J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN 13)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL031326; CAA20458.1;
 DR EMBL: AL161559; CAB79292.1;
 KW Hypothetical protein.
 SO SEQUENCE 745 AA; 83092 MW; 45BFA5A79B210299 CRC64;

Query Match 45.6%; Score 47; DB 10; Length 745;
 Best Local Similarity 47.1%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 GFNETSCLKILADGFEFE 17
 DB 289 GFNKTGCVNTLCGPFVO 305

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RESULT 12
ID Q9KRL7 PRELIMINARY; PRT: 568 AA.
AC Q9KRL7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RESPONSE REGULATOR.
OS VC1086.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR M16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
RA McDonald L., Ullrich T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL: AE004434; AAF96979.1; -.
DR TIGR: VC1086; -.
DR InterPro: IPR001789; -.
DR InterPro: IPR003588; -.
DR Pfam: PF00072; response_reg. 1.
DR SMART: SM00331; P2C_SIG: 1.
DR SEQUENCE 568 AA; 64331 MW; 87A02A350D986F51 CRC64;
SQ
Query Match 44.7%; Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 SCLTKLADGFFEF 18
DB 460 SSKETPDGFFEF 472

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DR Pfam: PF00309; Sigma54_factors; 1.
DR PRINTS: PR00045; SIGMA54_FCT.
DR PROSITE: PS00717; SIGMA54_1; 1.
DR PROSITE: PS00718; SIGMA54_2; 1.
DR PROSITE: PS50044; SIGMA54_3; 1.
KW DNA-binding; DNA-directed RNA polymerase; Sigma factor;
KW Transcription regulation.
SQ SEQUENCE 492 AA; 55359 MW; 8B95B2C7060DF7F7 CRC64;
Query Match 44.2%; Score 45.5; DB 2; Length 492;
Best Local Similarity 47.6%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 5; Indels 5; Gaps 1;
QY 3 NET-----SCLTKLADGFFEF 18
DB 353 NETLKYSKCIYKFGGFFEF 373

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RESULT 14
ID Q9XRE6 PRELIMINARY; PRT: 148 AA.
AC Q9XRE6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN OLA-DOA2.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MERINO;
RX MEDLINE=97083726; PubMed=8930070;
RA Escayg A.P., Hickford J.G., Montgomery G.W., Dodds K.G., Bullock D.W.;
RT "Polymorphism at the ovine major histocompatibility complex class II
RT loci."
RL Anim. Genet. 27:305-312(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MERINO;
RX Slow S., Ridgway H.J., Hickford J.G.H.;
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF129118; A033404.1; -.
DR HSSP: P01888; 18WG.
DR InterPro: IPR001003; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003597; -.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00993; MHC_II_alpha; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SMART: SM00407; IGc1. 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16852 MW; F31FE0608CD7ED07 CRC64;
Query Match 43.7%; Score 45; DB 7; Length 148;
Best Local Similarity 55.6%; Pred. No. 7.2;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 GNETSCLTKLADGFFEF 18
DB 111 GVSSTFLPKDDSFEEK 128

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RESULT 15
Q28403

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ID 028403      PRELIMINARY:      PRT:      207 AA.
AC 028403;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Euhydra lurtis (Sea otter).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Euhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66163018; PubMed=8575817;
  King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
  Stolt J.L., Ferrick D.A.;
  "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
  the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
  Southern sea otter (Euhydra lurtis nereis).";
  Immunogenetics 43:190-195(1996).
RL EMBL; LA6804; AAB01428.1; -.
DR HSSP; P05231; IL6.
DR InterPro; IPR003573; -.
DR InterPro; IPR003574; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFNGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
SO SEQUENCE 207 AA; 23527 MW; 729E0CD91136D8B CRC64;

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Query Match      43.7%; Score 45; DB 6; Length 207;
Best Local Similarity 38.9%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 2 ENETSCLAKLADGFEFE 19
DB 103 FMOETCLRITFGIADPO 120

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Search completed: October 4, 2001, 19:11:58
 Job time: 1184 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; search time 32.27 Seconds
(without alignments)
12.123 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105

Sequence: 1 GFNETSCLKADGFEFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 segs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Prd. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	185	3	US-09-122-443-16
2	61	59.2	162	2	US-08-716-317-10
3	61	59.2	163	2	US-08-716-317-15
4	61	59.2	164	1	US-08-318-193-60
5	61	59.2	167	1	US-08-246-427A-2
6	61	59.2	167	2	US-08-766-620-2
7	61	59.2	167	2	PCT-US95-06094-2
8	61	59.2	172	4	US-08-149-101A-21
9	61	59.2	172	5	PCT-US94-12873-21
10	61	59.2	174	4	US-08-149-101A-20
11	61	59.2	174	5	PCT-US94-12873-20
12	61	59.2	183	1	US-08-009-973-1
13	61	59.2	184	1	US-08-567-047-2
14	61	59.2	184	2	US-08-693-182-2
15	61	59.2	184	2	US-08-567-048-2
16	61	59.2	184	2	US-09-008-482-2
17	61	59.2	184	2	US-08-945-529-8
18	61	59.2	184	2	US-08-945-529-9
19	61	59.2	184	2	US-08-945-529-10
20	61	59.2	184	2	US-08-945-529-11
21	61	59.2	184	2	US-08-945-529-12
22	61	59.2	184	4	US-08-149-101A-17
23	61	59.2	184	4	US-08-149-101A-22
24	61	59.2	184	5	PCT-US94-12873-17
25	61	59.2	184	5	PCT-US94-12873-22
26	61	59.2	184	6	5186931-1
27	61	59.2	185	1	US-07-632-070B-1

28	61	59.2	185	1	US-07-918-181A-2	Sequence 2, Appl1
29	61	59.2	185	1	US-07-918-181A-4	Sequence 4, Appl1
30	61	59.2	185	1	US-07-918-181A-6	Sequence 6, Appl1
31	61	59.2	185	1	US-07-918-181A-8	Sequence 8, Appl1
32	61	59.2	185	1	US-08-231-575-2	Sequence 2, Appl1
33	61	59.2	185	1	US-08-231-575-4	Sequence 4, Appl1
34	61	59.2	185	1	US-08-231-575-6	Sequence 6, Appl1
35	61	59.2	185	1	US-08-231-575-8	Sequence 8, Appl1
36	61	59.2	185	1	US-08-246-427A-5	Sequence 5, Appl1
37	61	59.2	185	2	US-08-716-317-7	Sequence 7, Appl1
38	61	59.2	185	2	US-08-766-620-5	Sequence 5, Appl1
39	61	59.2	185	5	PCT-US92-05612-2	Sequence 5, Appl1
40	61	59.2	185	5	PCT-US93-06928-2	Sequence 2, Appl1
41	61	59.2	185	5	PCT-US93-06928-4	Sequence 4, Appl1
42	61	59.2	185	5	PCT-US93-06928-6	Sequence 6, Appl1
43	61	59.2	185	5	PCT-US93-06928-8	Sequence 8, Appl1
44	61	59.2	185	6	5186931-2	Patent No. 5186931
45	61	59.2	186	1	US-07-632-070B-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-122-443-16
Sequence 16, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTORINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-16
Query Match 100.0%; Score 103; DB 3; Length 185;
Best Local Similarity 100.0%; Prd. No. 1,2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GFNETSCLKADGFEFE 19
|||||

DB 68 GNETSCUKRLADGFEFE 86

RESULT 2

US-08-716-317-10

Sequence 10, Application US/08716317

Patent No. 5919654

GENERAL INFORMATION:

APPLICANT: HAMA, YUKO

APPLICANT: TOHDA, HIDEKI

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: NIKAI, KIYOKAZU

APPLICANT: KUMAGAI, HIROKICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/716,317

FILING DATE: 02-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIOR APPLICATION DATA: JP 17167/1995

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-716-317-10

Query Match 59.28; Score 61; DB 2; Length 162;

Best Local Similarity 57.9%; Pred. No. 0.0074;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

DB 55 GNETSCUKRLADGFEFE 73

RESULT 3

US-08-716-317-15

Sequence 15, Application US/08716317

Patent No. 5919654

GENERAL INFORMATION:

APPLICANT: HAMA, YUKO

APPLICANT: TOHDA, HIDEKI

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: NIKAI, KIYOKAZU

APPLICANT: KUMAGAI, HIROKICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/716,317

FILING DATE: 02-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIOR APPLICATION DATA: JP 17167/1995

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 163 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-716-317-15

APPLICANT: NIKAI, KIYOKAZU

APPLICANT: KUMAGAI, HIROKICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/716,317

FILING DATE: 02-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIOR APPLICATION DATA: JP 17167/1995

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 163 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-716-317-15

Query Match 59.28; Score 61; DB 2; Length 163;

Best Local Similarity 57.9%; Pred. No. 0.0075;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

DB 56 GNETSCUKRLADGFEFE 74

RESULT 4

US-08-318-193-60

Sequence 60, Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.

APPLICANT: MALEX, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: POLEY & LARDNER

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-193-60

Query Match 59.2%; Score 61; DB 1; Length 164;
Best Local Similarity 57.9%; Pred. No. 0.0075;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCKRLADGFEFE 19
DB 57 GFNETCLVAKITGLLEFE 75

RESULT 5
US-08-246-427A-2
Sequence 2, Application US/08246427A
Patent No. 5641657
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CECCHI, STEWART & OLSTEIN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-246-427A-2

Query Match 59.2%; Score 61; DB 2; Length 167;
Best Local Similarity 57.9%; Pred. No. 0.0077;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCKRLADGFEFE 19
DB 60 GFNETCLVAKITGLLEFE 78

RESULT 6
US-08-766-620-2
Sequence 2, Application US/08766620
Patent No. 5958400
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CECCHI, STEWART & OLSTEIN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,620
FILING DATE: December 12, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match 59.2%; Score 61; DB 2; Length 167;
Best Local Similarity 57.9%; Pred. No. 0.0077;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCKRLADGFEFE 19
DB 60 GFNETCLVAKITGLLEFE 78

DB 60 GNETCLVKITGLLEFE 78

RESULT 7

PCT-US95-06094-2

Sequence 2, Application PC/TUS9506094

GENERAL INFORMATION:

APPLICANT: RUBEN, ET AL.

TITLE OF INVENTION: Interleukin-6 splice variant

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06094

FILING DATE: Submitted herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/246,427

FILING DATE: MAY 19, 1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

PCT-US95-06094-2

Query Match 59.2%; Score 61; DB 5; Length 167;

Best Local Similarity 57.9%; Pred. No. 0.0077;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GNETSCLKLADGFEFE 19

DB 60 GNETCLVKITGLLEFE 78

RESULT 8

US-08-149-101A-21

Sequence 21, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,101A

FILING DATE: 8-No. 6171824-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/097,869

FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oster, Jeffrey B. and Paciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 172

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: homo sapien

US-08-149-101A-21

Query Match 59.2%; Score 61; DB 4; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GNETSCLKLADGFEFE 19

DB 78 GNETCLVKITGLLEFE 96

RESULT 9

PCT-US94-12873-21

Sequence 21, Application PC/TUS9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12873

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 172

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-12873-21

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GNETSCLKLADGFEFE 19

||||:||||:|
Db 78 GFNETCLVKITGLFEF 96

RESULT 10
US-08-149-101A-20
Sequence 20, Application US/08149101A
Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.
APPLICANT: Leung, David W.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cell Therapeutics, Inc.
STREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98119

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149/101A
FILING DATE: 6-No. 6171824-1993

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/097,869
FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oster, Jeffrey B. and Faciszewski, Stephen
REGISTRATION NUMBER: 32,585 and 36,131, respectively
REFERENCE/DOCKET NUMBER: 0103A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 174

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: no

ANTI-SENSE: no
FRAGMENT TYPE:

ORIGINAL SOURCE:
ORGANISM: homo sapien

US-08-149-101A-20

Query Match 59.2%; Score 61; DB 4; Length 174;
Best Local Similarity 57.9%; Pred. No. 0.008;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFPEF 19
||||:||||:|
Db 78 GFNETCLVKITGLFEF 96

RESULT 11
PCT-US94-12873-20
Sequence 20, Application PC/TUS9412873
GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44mb, double side, high density
COMPUTER: AST-IBM Compatible
OPERATING SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12873
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 174

TYPE: amino acid
TOPOLOGY: linear
PCT-US94-12873-20

Query Match 59.2%; Score 61; DB 5; Length 174;
Best Local Similarity 57.9%; Pred. No. 0.008;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFPEF 19
||||:||||:|
Db 78 GFNETCLVKITGLFEF 96

RESULT 12
US-08-009-973-1
Sequence 1, Application US/08009973
Patent No. 5338834

GENERAL INFORMATION:

APPLICANT: WILLIAMS, Ashley M.
TITLE OF INVENTION: Ultrapure Human Interleukin-6
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009,973
FILING DATE: 19930126

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/199 ALLE
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
US-08-009-973-1

Query Match 59.2%; Score 61; DB 1; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.0085;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFPEF 19
||||:||||:|
Db 76 GFNETCLVKITGLFEF 94

RESULT 13

US-08-567-047-2
Sequence 2, Application US/08567047
Patent No. 5789552
Patent No. 5789552, 5789555
GENERAL INFORMATION:
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
ANTAGONISTS AND SUPRAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,047
FILING DATE: 04-DEC-1995
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-047-2

Query Match 59.2%; Score 61; DB 1; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKRLADFFEEFEE 19
DB 77 GFNETCLVKITGLLEFE 95

RESULT 14
US-08-693-182-2
Sequence 2, Application US/08693182
Patent No. 5849283
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Genaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
ANTAGONISTS AND SUPRAGONISTS OF HUMAN
TITLE OF INVENTION: INTERLUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Netmark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A000805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CILIBERTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-182-2

Query Match 59.2%; Score 61; DB 2; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKRLADFFEEFEE 19
DB 77 GFNETCLVKITGLLEFE 95

RESULT 15
US-08-567-048-2
Sequence 2, Application US/08567048
Patent No. 5891998
GENERAL INFORMATION:
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Genaro
TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
ANTAGONISTS AND SUPRAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,048

Fri, Oct 5 10:02:10 2001

us-09-230-048-2_copy_87_105.raii

Page 7

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1          CILING DATE: 04-DEC-1995
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3          CLASSIFICATION: 530
4
5          PRIOR APPLICATION DATA:
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7          APPLICATION NUMBER:  US 08/387,924
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9          FILING DATE: 23-FEB-1995
10
11         APPLICATION NUMBER:  17 RM93A000403
12
13         FILING DATE: 23-JUN-1993
14
15         ATTORNEY/AGENT INFORMATION:
16
17         NAME:  BROWDY, Roger L.
18
19         REGISTRATION NUMBER:  25,618
20
21         REFERENCE/POCKET NUMBER:  SAVINO-1
22
23         TELECOMMUNICATION INFORMATION:
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25         TELEPHONE:  202-658-5197
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27         TELEFAX:  202-737-3528
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29         TELEX:  248633
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31         INFORMATION FOR SEQ ID NO:  2:
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33         SEQUENCE CHARACTERISTICS:
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35         LENGTH:  184 amino acids
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37         TYPE:  amino acid
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39         TOPOLOGY:  linear
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41         MOLECULE TYPE:  protein
42
43  US-08-567-048-2

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Query Match      59.2%; Score 61; DB 2; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Db      77 GENETCCLKVKITGLLEEE 95
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Search completed: October 4, 2001, 19:10:32
Job time: 1163 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:08 ; Search time 54.44 seconds
(without alignments)
236.082 Million cell updates/sec

Title: US-09-230-048-3

Sequence: 1 MNSFSTSAEGPYAFSLGLL.....LILRSFEFLQSSLRALROM 212

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Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1071	100.0	212	8	AA1970238
2	1071	100.0	212	9	AA1980269
3	1071	100.0	212	10	AA1990047
4	1071	100.0	212	10	AA1990371
5	1071	100.0	212	10	AA1990436
6	1071	100.0	212	10	AA1990459
7	1071	100.0	212	11	AA1990545
8	1071	100.0	212	14	AA1993430
9	1071	100.0	212	14	AA1993476
10	1071	100.0	212	15	AA1994041
11	1071	100.0	212	15	AA1994249

12	1071	100.0	212	16	AA1972317
13	1068	99.7	212	21	AA197816
14	1068	99.7	212	9	AA1981156
15	1065	99.4	212	9	AA1982577
16	1065	99.4	212	9	AA1981176
17	1065	99.4	212	10	AA1990121
18	1064	99.3	212	14	AA1993384
19	1063	99.3	212	22	AA199786
20	1066	97.7	212	12	AA1912521
21	1045	97.6	212	18	AA195878
22	1045	97.6	212	18	AA193643
23	1036	96.7	211	13	AA195279
24	1002.5	93.6	201	9	AA191162
25	955	88.2	188	20	AA195011
26	948	88.5	196	18	AA196848
27	943.5	88.1	208	9	AA191160
28	942	88.0	515	21	AA191544
29	938.5	87.6	543	20	AA193154
30	938	87.6	185	9	AA191159
31	938	87.6	185	11	AA1905275
32	938	87.6	185	15	AA1945717
33	938	87.6	185	16	AA1968624
34	938	87.6	186	9	AA1980270
35	938	87.6	186	16	AA1979339
36	938	87.6	186	16	AA197565
37	938	87.6	186	21	AA193220
38	938	87.6	187	12	AA1913471
39	938	87.6	317	16	AA1993321
40	938	87.6	317	22	AA1953202
41	938	87.6	347	22	AA1972222
42	937.5	87.5	208	10	AA194755
43	936	87.4	185	15	AA1945719
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45	934	87.2	184	15	AA195256

ALIGNMENTS

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DT	21-MAR-1980 (first entry)
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DE	Interferon-beta 2a.
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OS	Homo sapiens.
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PN	EP220574-A.
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PD	06-MAY-1987.
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PE	10-OCT-1986; 86EP-0114049.
XX	
FR	08-MAY-1986; 86US-0860893.
PR	14-OCT-1985; 85IL-0076714.
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PA	(YEDA) YEDA RES & DEV CO LTD.
XX	
PI	Revel M, Zilberstein A;
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DR	WPI: 1987-124210/18.
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DR	N-PSDB: AA1970348.
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PT	Recombinant human interferon-beta(2a) and beta(2b) - useful for
PT	inflammation, acute phase response or regulation of cell
PT	proliferation
XX	

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 mnsfstagpafslglvlpapfapvpgedskvaaaphqpltseserldkqiryi 60
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QY 61 LDGISAARKETCKSNMCKESSKEALAEENNLNLPKMAKDCGFCGSGFNEETCLVKIITGLL 120
 |||
 DB 61 ldgisalrketcksnmckesskealaennlnlpkmaekdcgfcgsgfneetclvkiitgll 120
 |||

QY 121 EFEVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKKAKNLDATTPPTNNASLITKIQ 180
 |||
 DB 121 efeyvleylnrfesseeqaravomstkvliqflqkxaknldattpdptnaslltkiq 180
 |||

QY 181 AONQWLODMTTHLILRSFKFELQSSLRALROM 212
 |||
 DB 181 aqnqwldmtthlilrsfkelfqsslraltrom 212
 |||

RESULT 4

AAP90371
 ID AAP90371 standard; protein; 212 AA.
 XX
 AC AAP90371;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE PBSF2-L8.
 XX
 KW Fc epsilon receptor; cloned gene; IGE; PBSF2-L8; allergy;
 KM asthma; BSF-2.
 PN EP321601-A.
 PD 28-JUN-1989.
 PF 22-DEC-1987; 87EP-0119080.
 PR 22-DEC-1987; 87EP-0119080.
 PA (OSAU) OSAKA UNIVERSITY.
 PI Kishimoto T, Sueamura M, Kikutani H, Barsumian E;
 DR WPI: 1989-186101/26.
 DR N-PSDB; AAN90134, AAN90135, AAN90136.
 XX
 PT Cloned genes coding for soluble IGE receptor - comprising modified coding
 XX sequence of Fc epsilon receptor gene.
 PS Disclosure: fig 3; 19pp; English.
 CC Peptide sequence of PBSF2-L8. See also AAN90134-6.
 XX
 SQ Sequence 212 AA.

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTAGCPVAFSLGLLVLPAPFAPVPGEDSKVAAAPHQPLTSSERIDKQIRYI 60
 |||
 DB 1 mnsfstagcpvafslglvlpapfapvpgedskvaaaphqpltseserldkqiryi 60
 |||

QY 61 LDGISAARKETCKSNMCKESSKEALAEENNLNLPKMAKDCGFCGSGFNEETCLVKIITGLL 120
 |||
 DB 61 ldgisalrketcksnmckesskealaennlnlpkmaekdcgfcgsgfneetclvkiitgll 120
 |||

QY 121 EFEVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKKAKNLDATTPPTNNASLITKIQ 180
 |||
 DB 121 efeyvleylnrfesseeqaravomstkvliqflqkxaknldattpdptnaslltkiq 180
 |||

QY 181 AONQWLODMTTHLILRSFKFELQSSLRALROM 212
 |||
 DB 181 aqnqwldmtthlilrsfkelfqsslraltrom 212
 |||

RESULT 5

AAP90436
 ID AAP90436 standard; peptide; 212 AA.
 XX
 AC AAP90436;
 XX
 DT 20-OCT-1989 (first entry)
 XX
 DE Interferon-beta-2.
 XX
 KW Interferon-beta-2; monoclonal antibodies; human;
 KW acute myelogenous leukaemia; breast cancer; bacterial and
 KW parasitic diseases; bone marrow transplants.
 XX
 OS Homo sapiens (human).
 XX
 PN EP326120-A.
 PD 02-AUG-1989.
 PF 25-JAN-1989; 89EP-0101295.
 PR 26-JAN-1988; 88IL-0088376.
 PA (YEDA) YEDA RESEARCH AND DEV CO LTD.
 PI Revel M, Rubinstein M, Mory Y, Chen L, Novick D, Michalevycz R;
 DR WPI: 1989-222084/31.
 DR N-PSDB; AAN90377.
 XX
 PT Monoclonal antibody to human interferon-beta-2
 PT - produced by hybridoma cell line and useful for leukaemia
 PT treatment etc.
 PS Disclosure: fig 1; 26 pp; English.
 CC Interferon-beta-2 (see AAN90377). Used to make
 CC monoclonal antibodies, and in the treatment of the diseases
 CC in KW above.
 XX
 SQ Sequence 212 AA.

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTAGCPVAFSLGLLVLPAPFAPVPGEDSKVAAAPHQPLTSSERIDKQIRYI 60
 |||
 DB 1 mnsfstagcpvafslglvlpapfapvpgedskvaaaphqpltseserldkqiryi 60
 |||

QY 61 LDGISAARKETCKSNMCKESSKEALAEENNLNLPKMAKDCGFCGSGFNEETCLVKIITGLL 120
 |||
 DB 61 ldgisalrketcksnmckesskealaennlnlpkmaekdcgfcgsgfneetclvkiitgll 120
 |||

QY 121 EFEVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKKAKNLDATTPPTNNASLITKIQ 180
 |||
 DB 121 efeyvleylnrfesseeqaravomstkvliqflqkxaknldattpdptnaslltkiq 180
 |||

QY 181 AONQWLODMTTHLILRSFKFELQSSLRALROM 212
 |||
 DB 181 aqnqwldmtthlilrsfkelfqsslraltrom 212
 |||

```

RESULT 6
ID AAP90469 standard; protein; 212 AA.
XX
AC AAP90469;
XX
DE 01-NOV-1989 (first entry)
XX
DE Interleukin-6.
XX
XX Interleukin-6: lysine-depleted variant;
XX site-directed mutagenesis; human.
XX
OS Homo sapiens.
XX
PN W08905824-A.
XX
PD 29-JUN-1989.
XX
PF 22-DEC-1988; 88WO-US04633.
XX
PR 23-DEC-1987; 87US-0137043.
XX
PA (GENE ) GENETICS INST INC.
XX
PI Shaw G;
XX
DR WPI: 1989-206594/28.
XX N-PSDB: AAN90255.
XX
PT New lysine depleted variants of polypeptide
XX -opt, modified with hydrophilic residues,
XX biologically active but with altered solubility, stability etc.
XX
XX Disclousure: fig 3; 35pp; English.
XX
CC DNA of interleukin-6 (see corresp. AAN90255). Used in the patent
XX to create lysine depleted variants by site-directed mutagenesis,
XX or synthesis.
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 4,5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTAFGCVAFSLGLLVLPAPFPAPVPPEGDSKDVAAPHRQPLTSSERIDKQIRYI 60
DB 1 mnsfstafgcvafslgllvlpafpfpvppgedskdvaaphrpltsesridkqiryi 60
OY 61 LDGTSALRKETCNKSNKCESSKEALAEENNLPRKMAEKDGCFOGSENEETCLVKTITGL 120
DB 61 ldgtsalrketcnksnkcesskealaeennlprkmaekdgcfogsfneetclvktitgll 120
OY 121 EFREYVLEYLQNRPFSSSEQARAVQNSTKVLIOFLQKAKNLDAITTPPTNASILTKLQ 180
DB 121 efreyvleylqnrpfssseeqaravqnmstkvliflqkknldaittpptnaailltklq 180
OY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
DB 181 aqngwldmtthlilrsfkeflqslralrqlm 212
DE 181 aqngwldmtthlilrsfkeflqslralrqlm 212

RESULT 7
ID AAR05415 standard; protein; 212 AA.
XX
AC AAR05415;
XX
DE 27-JUL-1990 (first entry)
XX

```

```

XX
DE Human B-cell differentiation factor gene product.
XX
XX BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
XX
OS Homo sapiens.
XX
PN JP02009388-A.
XX
PD 12-JAN-1990.
XX
PF 08-JUL-1988; 88JP-0170142.
XX
PR 09-MAR-1988; 88JP-0055270.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI: 1990-055348/08.
XX N-PSDB: AAO01763.
XX
PT physiologically active protein prepn.
XX by transforming plasmid having gene coding physiologically
XX active protein and gene of dihydrofolic acid reductase to hamster
XX ovary etc.
XX
XX Example 3; Fig 6; 12pp; Japanese.
XX
CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
XX with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product
XX is a B-cell differentiating factor.
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 4,5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTAFGCVAFSLGLLVLPAPFPAPVPPEGDSKDVAAPHRQPLTSSERIDKQIRYI 60
DB 1 mnsfstafgcvafslgllvlpafpfpvppgedskdvaaphrpltsesridkqiryi 60
OY 61 LDGTSALRKETCNKSNKCESSKEALAEENNLPRKMAEKDGCFOGSENEETCLVKTITGL 120
DB 61 ldgtsalrketcnksnkcesskealaeennlprkmaekdgcfogsfneetclvktitgll 120
OY 121 EFREYVLEYLQNRPFSSSEQARAVQNSTKVLIOFLQKAKNLDAITTPPTNASILTKLQ 180
DB 121 efreyvleylqnrpfssseeqaravqnmstkvliflqkknldaittpptnaailltklq 180
OY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
DB 181 aqngwldmtthlilrsfkeflqslralrqlm 212

RESULT 8
ID AAR33430 standard; protein; 212 AA.
XX
AC AAR33430;
XX
DE 28-JUL-1993 (first entry)
XX
DE IFN-beta-2a.
XX
XX Interferon; IFN; pharmaceutical; inflammation; acute phase response;
XX regulation; cell; proliferation; inhibition; fibroblast; sclerosis;
XX infection; antiviral; antitumour; human; IFN-beta-1; IFN-beta-2;
XX IFN-beta-2a; IFN-beta-2b.
XX
OS Homo sapiens.
XX
PN EP536520-A.
XX

```

XX 14-APR-1993.
 PD 10-OCT-1986; 86EP-0114478.
 XX 14-OCT-1985; 85IL-0076714.
 PR 08-MAY-1986; 86DS-0860883.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX
 PI Revel M, Zilberstein A;
 XX
 DR WPI: 1993-118821/15.
 DR N-PSDB: AA039582.
 PT New compsn. contg. human interferon-beta 2A - for treating
 PT inflammation and acute phase response, regulating cell
 PT proliferation, etc.
 XX
 PS Disclosure: Fig 1: 16pp: English.
 CC This sequence represents interferon (IFN)-beta-2a. This protein was
 CC used in the construction of a pharmaceutical composition which was
 CC used for treating inflammation, acute phase response, regulation of
 CC cell proliferation, inhibition of fibroblast proliferation and for
 CC prevention of sclerosis after infection. IFNs are important antiviral
 CC and antitumor proteins produced by the human body. The major species
 CC of IFN produced by human fibroblasts is IFN-beta-1. This is immuno-
 CC logically distinct from IFN-beta-2. Two genes have been found to
 CC encode IFN-beta-2, IFN-beta-2a and IFN-beta-2b.
 XX
 SQ Sequence 212 AA;
 Query Match 100.0%; Score 1071; DB 14; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4,5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNSFSTSAAGPVAFSIGLLVLPAAFPAPVPPEGDSKDVAAAPRHOPLTSSERIDKQIRYI 60
 DB 1 mnsfstsaagpvaafsiggllvlpaafpapvppegdskdvaaprhoptlsseridkqiryi 60
 QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCFOSGFNEETCLVKITIGLL 120
 DB 61 ldgisalrketcnksnmcesskealaennllpkmaekdcfsgfneetclvkitigll 120
 QY 121 EFEVYLEYIQNRFESSEEDARAVOMSTKVLIOFLQKAKAKNDATTTPDPTNNSLITKIQ 180
 DB 121 efevyleyiqnrfesseedaravomstkvliqflqkakakndalttppdptnaslilkqi 180
 QY 181 AQNQWLQDMTTHLILRSFKEFLQSSIRALROM 212
 DB 181 aqnqwlqdmthlllrskfqlsirlalrqm 212
 RESULT 9
 AAR34726
 ID AAR34726 standard; protein: 212 AA.
 XX
 AC AAR34726;
 XX
 DT 24-AUG-1993 (first entry)
 XX
 DE Human IL-6 (for modification).
 XX
 KW Interleukin-6; stability; blood; cytokine; BSF-2.
 OS Homo sapiens.
 XX
 PH Key
 FT Peptide 1..29 Location/Qualifiers
 FT /label= sig_pep
 FT Protein 30..212

FT /label= mat_protein
 XX JP0508609-A.
 PN 06-APR-1993.
 PD 31-JUL-1991; 91UP-0191475.
 PF 31-JUL-1990; 90JP-0204440.
 PR (TORA) TORAY IND INC.
 PA
 XX
 DR WPI: 1993-149232/18.
 DR
 XX
 PT Modified interleukin-6 derivs. - used to treat platelet-reducing
 PT conditions, thrombocytopenia
 PT
 XX
 PS Claim 1: Page 2; 6pp: Japanese.
 CC A modified interleukin-6 (IL-6) contg. at least 3 sequences of Asn-X-
 CC Thr or Asn-X-Ser, where X is an amino acid other than Pro, is
 CC claimed (no specific sequences, nor the sequence below are given
 CC in the specification 1).
 CC The modified IL-6 can be expected to have higher stability in
 CC blood, higher medical effect and higher absorption in the
 CC objective organ.
 XX
 SQ Sequence 212 AA;
 Query Match 100.0%; Score 1071; DB 14; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4,5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNSFSTSAAGPVAFSIGLLVLPAAFPAPVPPEGDSKDVAAAPRHOPLTSSERIDKQIRYI 60
 DB 1 mnsfstsaagpvaafsiggllvlpaafpapvppegdskdvaaprhoptlsseridkqiryi 60
 QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCFOSGFNEETCLVKITIGLL 120
 DB 61 ldgisalrketcnksnmcesskealaennllpkmaekdcfsgfneetclvkitigll 120
 QY 121 EFEVYLEYIQNRFESSEEDARAVOMSTKVLIOFLQKAKAKNDATTTPDPTNNSLITKIQ 180
 DB 121 efevyleyiqnrfesseedaravomstkvliqflqkakakndalttppdptnaslilkqi 180
 QY 181 AQNQWLQDMTTHLILRSFKEFLQSSIRALROM 212
 DB 181 aqnqwlqdmthlllrskfqlsirlalrqm 212
 RESULT 10
 AAR49041
 ID AAR49041 standard; protein: 212 AA.
 XX
 AC AAR49041;
 XX
 DT 06-SEP-1994 (first entry)
 XX
 DE Human Interleukin-6.
 XX
 KW Interleukin 6; IL-6; thrombocytopenia; surgery; chemotherapy;
 KW radiation therapy; bone marrow transplantation; cancer therapy;
 KW neoplasia; anti-neoplastic activity.
 OS Homo sapiens.
 XX
 PN W09403492-A.
 XX
 PD 17-FEB-1994.
 XX
 PF 01-JUL-1993; 93WO-AU00324.

PR 06-AUG-1992; 92AU-0003983.
 XX (LUDM-) LUDMIG INST CANCER RES.
 PA (UTME) UNIV MELBOURNE.
 XX
 PI Simpson RJ, Williams NT;
 XX
 DR WPI: 1994-065607/08.
 DR N-PSDB: AA055973.
 XX
 PR New interleukin-6 variants - capable of stimulating
 PT chromocytopenias while exhibiting low hybridoma growth factor
 PT activity
 XX
 PS Disclosure; Page 33; 46pp; English.
 XX
 CC This sequence is human interleukin-6 (IL-6). IL-6 variants in
 CC the form of non-full length molecules can stimulate, enhance or
 CC facilitate chromocytopenias without the side effects of other IL-6
 CC activators. The IL-6 variants are useful for inducing
 CC chromocytopenias in chromocytopenic patients following surgery,
 CC chemotherapy, radiation therapy or bone marrow transplantation. The
 CC IL-6 variants may also be useful in cancer therapy where the
 CC fragments express anti-neoplastic activity.

Sequence 212 AA:

Query Match 100.0%; Score 1071; DB 15; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFCVAFSLCLLVLPAPAPAPVPCEDSKDYAAPHRPPLTSSRIDKQIRYI 60
 DB 1 mnsfstsfgyvatslgllivlpafpapyppgedskdyaphrpltsesridkqiryi 60
 OY 61 LDGTSALRKETCKSNKCESSKALAEENNLPKMAEKDGCQSFNFTCLVITIGLL 120
 DB 61 ldgtsalrketcnksnkcscskalaennlppkmaekdcqsfneftclvllcgll 120
 OY 121 EFERYLLEYLQNRFFSESEQARAVQSTKYLIQFLQKKAKNLDATITPTPTNASLTKIQ 180
 DB 121 eferylleylqnrffsesegaravqsmtkvllqflqkknldatitptptnasllcklq 180
 OY 181 AQNQLDMTHLILRSFKEFLQSSRALROM 212
 DB 181 aqnqwlqdmthllrsfkeflqsslrarqm 212

RESULT 11

AA049249
 ID AAR49249 standard; Protein; 212 AA.

AC AAR49249;

DT 15-SEP-1994 (first entry)

XX Sequence of human B-cell differentiation factor (BCDF) encoded by
 DE cDNA.

XX B-cell differentiation factor; BCDF; antitumour; antiviral;
 KW lymphokine.

OS Homo sapiens.

XX EP585957-A.

PD 09-MAR-1994.

XX 06-AUG-1987; 87EP-0111409.

PR 06-AUG-1986; 86JP-0184058.

PR 27-AUG-1986; 86JP-0200433.

PR 18-DEC-1986; 86JP-0302659.
 PR 13-MAY-1987; 87JP-0116332.

XX (AJIN) AJINOMOTO KK.

PA (KISH/) KISHIMOTO T.

PI Akiyama Y, Hirano T, Kishimoto T, Matsui H, Okano A;
 XX Takahara Y;

DR WPI: 1994-076278/10.

DR N-PSDB: AA036265.

PT New non-glycosylated human B-cell differentiation factor -
 PT lacking signal sequence and produced in bacteria, useful as
 PT immuno therapeutic for stimulating antibody prodn, treating
 PT cancer etc, also DNA encoding it

PS Claim 2; Fig 5; 63pp; English.

CC Human T cells transformed by human T cell leukaemia virus (HTLV)
 CC produce BCDF which has an activity of 5x10(6) units/ml or more. For
 CC its prepn., RNA is extracted from human T cell line VT-1 (IFO 50096)
 CC and used to construct a cDNA library. Oligos are constructed from
 CC known N-terminal sequence of BCDF and used to screen the library.
 CC One positive clone, contg. plasmid bpsf2-38, was selected and
 CC sequenced. It includes the codons for an additional 28 AA N-terminal
 CC region. A polypeptide corresp. to AAs 28-212 of AAR49249, and a
 CC recombinant DNA comprising a gene encoding it are claimed.

Sequence 212 AA:

Query Match 100.0%; Score 1071; DB 15; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFCVAFSLCLLVLPAPAPAPVPCEDSKDYAAPHRPPLTSSRIDKQIRYI 60
 DB 1 mnsfstsfgyvatslgllivlpafpapyppgedskdyaphrpltsesridkqiryi 60
 OY 61 LDGTSALRKETCKSNKCESSKALAEENNLPKMAEKDGCQSFNFTCLVITIGLL 120
 DB 61 ldgtsalrketcnksnkcscskalaennlppkmaekdcqsfneftclvllcgll 120
 OY 121 EFERYLLEYLQNRFFSESEQARAVQSTKYLIQFLQKKAKNLDATITPTPTNASLTKIQ 180
 DB 121 eferylleylqnrffsesegaravqsmtkvllqflqkknldatitptptnasllcklq 180
 OY 181 AQNQLDMTHLILRSFKEFLQSSRALROM 212
 DB 181 aqnqwlqdmthllrsfkeflqsslrarqm 212

RESULT 12

AA072317
 ID AAR72317 standard; Protein; 212 AA.

AC AAR72317;

DT 14-NOV-1995 (first entry)

XX Interferon-beta2A.

XX biologically active; interferon-beta2a; IFN-beta2a; cell growth;
 KW terminal differentiation; cancer; inhibit fibroblast proliferation.

OS Homo sapiens.

XX EP645452-A.

PD 29-MAR-1995.

PR 10-OCT-1986; 86EP-0114478.

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XX 14-OCT-1985; 85IL-0076714.
PR 08-MAY-1986; 86US-0860883.
XX (YEDA ) YEDA RES & DEV CO LTD.
PA
PI Revel M, Zilberstein A;
XX WPI: 1995-124593/17.
DR N-PSDB; AAO86523.
XX
PT A DNA sequence encoding active interferon beta2a - used in the
PT proth. of the protein for the treatment of cancer, by inhibition
PT of fibroblast proliferation
XX
PS Claim 1; Fig 1; 17pp; English.
XX
CC Biologically active, interferon-beta2a (IFN-beta2a), including the
CC N-terminus of the mature protein, may be used to influence cell growth
CC and differentiation esp. terminal differentiation of cancer cells and
CC to inhibit fibroblast proliferation preventing sclerosis after
CC infection.
XX
SQ Sequence 212 AA;
XX
Query Match 100.0%; Score 1071; DB 16; Length 212;
Best Local Similarity 100.0%; Pred. No. 4,5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MNSFSTSAFGPAVFSIGLLVLPAAFPAPVPPGSDSKDVAAPHROPJTSSERIDKQIRYI 60
DB 1 mnsfststgpaafsigllvlvlpaafpapvpvgdskdvaaphrptltsseridkqiryi 60
XX
OY 61 LDGISALRKETCNKSNMCESSKREALAENNINLPRMAEKDCFGSGFNEETCLVKIITGL 120
DB 61 ldgisalrketcnksnmcesskreaennlnlprmaekdcfgsgfneetclvklitgll 120
XX
OY 121 EFEEVLEYLQNFESSEBOARVOMSTKVLIOFLQKKAKNLDAITTPDPTNASILTKLQ 180
DB 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
XX
OY 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
DB 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
XX
OY 181 AONQWLQDMTTHLILRSFKFLOSSLRALROM 212
DB 181 aqnqwlqdmthlilrsfkfloslralrom 212
XX
RESULT 13
AA87816
ID AAY87816 standard; Protein: 212 AA.
AC AAY87816;
XX
DT 24-AUG-2000 (first entry)
XX
DE Human IL-6 protein.
XX
NM NNT-1; human; neurotrophic factor; neurotrophic; neuroprotective; treatment;
KM anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
KM nervous system degeneration; Alzheimer's disease; Parkinson's disease;
KM amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KM Huntington's disease; peripheral neuropathy; neural retina degeneration;
KM retinopathy; immune disorder; hematopoietic disorder; IL-6.
XX
XX Homo sapiens.
XX OS
XX PN US6054294-A.
XX
PD 25-APR-2000.
XX
PF 12-DEC-1997; 97US-0988819.
XX
PR 03-FEB-1997; 97US-0792019.

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XX (AMGE-) AMGEN INC.
XX Chang M;
XX WPI: 2000-338492/29.
XX
PT New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage
XX
PS Example VIII; Fig 6; 42pp; English.
XX
CC This invention describes a novel nucleic acid molecule (I) encoding a
CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC ophthalmological activity. (I) is useful for producing NNT-1
CC polypeptides which are useful for treating patients in whom various
CC cells of the central, autonomic, or peripheral nervous system have
CC degenerated and/or have been damaged by congenital disease, trauma,
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC disease, peripheral neuropathy induced by diabetes or other metabolic
CC disorders, and/or dystrophies or degeneration of the neural retina such
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC night blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (I) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence represents the human IL-6 protein which is
CC described in the method of the invention.
XX
SQ Sequence 212 AA;
XX
Query Match 100.0%; Score 1071; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 4,5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MNSFSTSAFGPAVFSIGLLVLPAAFPAPVPPGSDSKDVAAPHROPJTSSERIDKQIRYI 60
DB 1 mnsfststgpaafsigllvlvlpaafpapvpvgdskdvaaphrptltsseridkqiryi 60
XX
OY 61 LDGISALRKETCNKSNMCESSKREALAENNINLPRMAEKDCFGSGFNEETCLVKIITGL 120
DB 61 ldgisalrketcnksnmcesskreaennlnlprmaekdcfgsgfneetclvklitgll 120
XX
OY 121 EFEEVLEYLQNFESSEBOARVOMSTKVLIOFLQKKAKNLDAITTPDPTNASILTKLQ 180
DB 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
XX
OY 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
DB 121 efeyvleylqnfessesboaravomstkvliqflqkkaknlda ittpdptnasiltklq 180
XX
OY 181 AONQWLQDMTTHLILRSFKFLOSSLRALROM 212
DB 181 aqnqwlqdmthlilrsfkfloslralrom 212
XX
RESULT 14
AAP81156
ID AAP81156 standard; Protein: 212 AA.
AC AAP81156;
XX
DT 15-OCT-1990 (first entry)
XX
DE Human B-cell differentiation factor (BCDF).
XX
KM B-cell differentiation factor; BCDF; cancer; autoimmune.
XX
XX Homo sapiens.
XX OS
XX PN EP257406-A.

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XX 02-MAR-1988.
PD
XX
XX 06-AUG-1988; 88EP-0111409.
XX
XX 06-AUG-1986; 86JP-0184058.
XX
XX 27-AUG-1986; 86JP-0200433.
XX
XX 18-DEC-1986; 86JP-0302699.
XX
XX 13-MAY-1987; 87JP-0116332.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
XX
XX WPI: 1988-057698/09.
XX
XX N-PSDB: AAN81460.
XX
XX Puffed polypeptide with B-cell differentiation factor activity -
XX
XX useful in prodn. of antibodies for diagnosis and therapy of
XX
XX cancers, infectious diseases etc.
XX
XX Claim 24; Fig 5; 72pp; English.
XX
XX BCDP may be used in the production and repair of B-cells, it is
XX
XX useful in treatment of autoimmune diseases, malignant tumors and
XX
XX may be used to influence B-cells to produce Abs in vitro.
XX
XX Sequence 212 AA:
XX

```

```

Query Match 99.7%; Score 1068; DB 9; Length 212;
Best Local Similarity 99.5%; Pred. No. 8.8e-97;
Matches 211; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFTSAGFVAFSLGLLVLPAAPFAPVPPGDSKDVAAAPHROPITSSERIDKQIRYI 60
DB 1 mnsftsaigvafslgllvlvpaafpavppgdskdvaaphrptlsseridkqlryl 60
OY 61 LDGISALRKETCKNSKNCSSKEALAEENLNLPKMAEKDCGSCGFNEETCLVYITGGL 120
DB 61 ldgisalrkctcknskncsskcalaeennlnpkmaekdcgscgfneetclvltgll 120
OY 121 EFEEYLEYLONRESSSEQARAVQSTKVLIOFLQKAKKNDATITPPPTTNASLTKLQ 180
DB 121 efeyleylgnrtesseeqaravqstkvliqflqkakkndaittppttnasltklq 180
OY 181 AQNQWLDQMTTHLLRSFKFLOSSLRALROM 212
DB 181 aqnqwlqdmthlllrsfkflosslralfqm 212

```

```

RESULT 15
AAP82577
ID AAP82577 standard: protein: 212 AA.
XX
XX AAP82577:
XX
XX 05-NOV-1990 (first entry)
XX
XX Leader sequence of of BSF from pBSF2-18.
XX
XX Lymphocyte: Immunoglobulin E; receptor; IGE; water soluble; allergy;
XX
XX pcEM4; signal sequence.
XX
XX Homo sapiens.
XX
XX EP286700-A.
XX
XX 19-OCT-1988.
XX
XX 11-NOV-1987; 87EP-0105425.
XX
XX 11-NOV-1987; 87EP-0105425.
XX

```

```

XX (OSAKI ) OSAKI UNIVERSITY.
XX
XX Kishimoto T, Suemura H, Barsumian, EL;
XX
XX WPI: 1988-308661/44.
XX
XX N-PSDB: AAN80966.
XX
XX Recombinant lymphocyte immunoglobulin E receptor fragments - useful
XX
XX as antiallergic agents.
XX
XX Disclosure; : p; English.
XX
XX The plasmid was prepd. from plasmid pBSF2-38 (Nature 324 73-76 (1986)).
XX
XX A fragment contg. the code for the BSF2 leader sequence was cloned
XX
XX into pGEM4. DNA encoding Fc-epsilon-R-1 was then ligated into this
XX
XX plasmid to produce a plasmid for the expression of water sol. receptor
XX
XX fragments useful in treating local or systemic IGE-mediated allergic
XX
XX reactions. They are glycosylated and so are biologically active.
XX
XX See also AAP82576.
XX
XX Sequence 212 AA:
XX

```

```

Query Match 99.4%; Score 1065; DB 9; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.7e-96;
Matches 211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNSFTSAGFVAFSLGLLVLPAAPFAPVPPGDSKDVAAAPHROPITSSERIDKQIRYI 60
DB 1 mnsftsaigvafslgllvlvpaafpavppgdskdvaaphrptlsseridkqlryl 60
OY 61 LDGISALRKETCKNSKNCSSKEALAEENLNLPKMAEKDCGSCGFNEETCLVYITGGL 120
DB 61 ldgisalrkctcknskncsskcalaeennlnpkmaekdcgscgfneetclvltgll 120
OY 121 EFEEYLEYLONRESSSEQARAVQSTKVLIOFLQKAKKNDATITPPPTTNASLTKLQ 180
DB 121 efeyleylgnrtesseeqaravqstkvliqflqkakkndaittppttnasltklq 180
OY 181 AQNQWLDQMTTHLLRSFKFLOSSLRALROM 212
DB 181 aqnqwlqdmthlllrsfkflosslralfqm 212

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Search completed: October 4, 2001, 18:52:09
Job time: 1675 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; Search time 32.27 seconds
(without alignments) 135.270 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAAGPVAFLGLL.....LUNSPKFLQSSLRALRQM 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/laa/5A.COMB.pep:*
4: /cgn2_6/ptodata/2/laa/5B.COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/2/laa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1071	100.0	212	1	US-08-792-019B-9
2	1071	100.0	212	3	US-08-988-819-9
3	1071	100.0	212	4	US-09-016-534-9
4	1071	100.0	212	4	US-08-097-869-7
5	1071	100.0	212	4	US-08-795-473B-6
6	1071	100.0	212	6	5510472-2
7	955	89.2	188	3	US-09-122-443-12
8	938	87.6	185	1	US-07-632-070B-1
9	938	87.6	185	1	US-07-918-181A-2
10	938	87.6	185	1	US-08-231-575-2
11	938	87.6	185	1	US-08-246-427A-5
12	938	87.6	185	2	US-08-766-620-5
13	938	87.6	185	5	PCT-US93-06928-2
14	938	87.6	185	6	5186931-2
15	938	87.6	186	1	US-07-632-070B-2
16	938	87.6	186	1	US-07-745-382-20
17	938	87.6	186	1	US-07-921-848-20
18	938	87.6	186	1	US-08-165-301A-20
19	938	87.6	186	3	US-08-469-318-163
20	938	87.6	186	3	US-08-468-609A-163
21	938	87.6	186	4	US-08-410-436-20
22	938	87.6	186	5	PCT-US94-14179-20
23	938	87.6	186	5	PCT-US95-01185-163
24	938	87.6	187	1	US-07-632-070B-3
25	938	87.6	317	3	US-08-469-318-145
26	938	87.6	317	3	US-08-468-609A-145
27	938	87.6	317	5	PCT-US95-01185-145

28	936	87.4	185	1	US-07-918-181A-6	Sequence 6, Appl 1
29	936	87.4	185	5	US-08-231-575-6	Sequence 6, Appl 1
30	936	87.4	185	5	PCT-US93-06928-6	Sequence 6, Appl 1
31	934	87.2	184	1	US-08-567-047-2	Sequence 2, Appl 1
32	934	87.2	184	2	US-08-567-048-2	Sequence 2, Appl 1
33	934	87.2	184	6	5186931-1	Patent No. 5186931
34	934	87.2	185	2	US-08-716-317-7	Sequence 7, Appl 1
35	932	87.0	185	1	US-07-918-181A-4	Sequence 4, Appl 1
36	932	87.0	185	1	US-08-231-575-4	Sequence 4, Appl 1
37	932	87.0	185	5	PCT-US93-06928-4	Sequence 4, Appl 1
38	930	86.8	185	1	US-07-918-181A-8	Sequence 8, Appl 1
39	930	86.8	185	1	US-08-231-575-8	Sequence 8, Appl 1
40	930	86.8	185	5	PCT-US93-06928-8	Sequence 8, Appl 1
41	929	86.7	184	2	US-08-693-182-2	Sequence 2, Appl 1
42	929	86.7	184	2	US-09-008-482-2	Sequence 2, Appl 1
43	927	86.6	183	1	US-08-009-973-1	Sequence 1, Appl 1
44	920	85.9	319	5	PCT-US94-04208-2	Sequence 2, Appl 1
45	918	85.7	185	5	PCT-US92-05612-2	Sequence 2, Appl 1

ALIGNMENTS

```
RESULT 1
US-08-792-019B-9
; Sequence 9, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
;
* US-08-792-019B-9
Query Match 100.0%; Score 1071; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MNSFSTSAAGPVAFLGLLVLVPAAPVPPGDSKDVAAAPROPPLTSSERDKQIRYI 60
|||||
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Db 1 MNSFSTAFGVPVAFSLGLLLVLPAPAPVPPEGDESKDYAAPHRQPLTSSERIDKQIRYI 60
QY 61 LDG|SALRK|ETCKNSNM|C|SSK|EAL|A|ENN|LN|PKMAEKDGC|FOS|GFNE|ETC|LV|IT|G|L 120
Db 61 LDG|SALRK|ETCKNSNM|C|SSK|EAL|A|ENN|LN|PKMAEKDGC|FOS|GFNE|ETC|LV|IT|G|L 120
QY 121 E|E|V|Y|L|E|I|O|N|R|E|S|S|E|O|A|R|A|V|O|M|S|T|K|V|I|O|F|L|O|K|K|A|N|L|D|A|I|T|T|P|D|P|T|N|A|S|L|T|R|K|Q 180
Db 121 E|E|V|Y|L|E|I|O|N|R|E|S|S|E|O|A|R|A|V|O|M|S|T|K|V|I|O|F|L|O|K|K|A|N|L|D|A|I|T|T|P|D|P|T|N|A|S|L|T|R|K|Q 180
QY 181 A|O|N|O|M|D|M|T|H|L|R|S|F|K|E|F|L|O|S|S|L|R|A|L|R|O|M 212
Db 181 A|O|N|O|M|D|M|T|H|L|R|S|F|K|E|F|L|O|S|S|L|R|A|L|R|O|M 212
RESULT 2
US-08-988-819-9
Sequence 9, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-988-819-9
Query Match 100.0%; Score 1071; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 E|E|V|Y|L|E|I|O|N|R|E|S|S|E|O|A|R|A|V|O|M|S|T|K|V|I|O|F|L|O|K|K|A|N|L|D|A|I|T|T|P|D|P|T|N|A|S|L|T|R|K|Q 180
Db 121 E|E|V|Y|L|E|I|O|N|R|E|S|S|E|O|A|R|A|V|O|M|S|T|K|V|I|O|F|L|O|K|K|A|N|L|D|A|I|T|T|P|D|P|T|N|A|S|L|T|R|K|Q 180
QY 181 A|O|N|O|M|D|M|T|H|L|R|S|F|K|E|F|L|O|S|S|L|R|A|L|R|O|M 212
Db 181 A|O|N|O|M|D|M|T|H|L|R|S|F|K|E|F|L|O|S|S|L|R|A|L|R|O|M 212
RESULT 3
US-09-016-534-9
Sequence 9, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-09-016-534-9
Query Match 100.0%; Score 1071; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 EEFVYLEYQNPFESSEEDARAVOMSTKVLQFLOKAKKNDLITPPDPTNLSLTKIQ 180
181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212

RESULT 4

US-08-097-869-7
Sequence 7, Application US/08097869
Patent No. 6204364
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 345 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,869
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,178
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24455-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-097-869-7

Query Match 100.0%; Score 1071; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MNSFSTSAFGPAVAFSLGLLVLPAPFAPVPFGSDSDVAAPHROPITSSERIDKQIRYI 60
1 MNSFSTSAFGPAVAFSLGLLVLPAPFAPVPFGSDSDVAAPHROPITSSERIDKQIRYI 60
DB 61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
DB 61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
DB 121 EEFVYLEYQNPFESSEEDARAVOMSTKVLQFLOKAKKNDLITPPDPTNLSLTKIQ 180
121 EEFVYLEYQNPFESSEEDARAVOMSTKVLQFLOKAKKNDLITPPDPTNLSLTKIQ 180
DB 181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
DB 181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
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RESULT 5

US-08-795-473B-6
Sequence 6, Application US/08795473B
Patent No. 6217858
GENERAL INFORMATION:
APPLICANT: Galun, Elhan
APPLICANT: Nahol, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
HEPATITIS B VIRUS (HBV) INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-08-795-473B-6

Query Match 100.0%; Score 1071; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MNSFSTSAFGPAVAFSLGLLVLPAPFAPVPFGSDSDVAAPHROPITSSERIDKQIRYI 60
1 MNSFSTSAFGPAVAFSLGLLVLPAPFAPVPFGSDSDVAAPHROPITSSERIDKQIRYI 60
DB 61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
DB 61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
61 LDGIALRKRETCNKSNCMCESSKEALAEENNLNLPMAEKDCFOSGFNEETCLVKIITGILL 120
DB 121 EEFVYLEYQNPFESSEEDARAVOMSTKVLQFLOKAKKNDLITPPDPTNLSLTKIQ 180
121 EEFVYLEYQNPFESSEEDARAVOMSTKVLQFLOKAKKNDLITPPDPTNLSLTKIQ 180
DB 181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
DB 181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212
181 AONQWLODMTTHLILRSKFEFLQSSLRALROM 212

RESULT 6

US10472-2
Patent No. 5510472
APPLICANT: REVEL, MICHEL, TIOUAI, PIERRE
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
INTERFERON-BETA2
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/883,633

FILED DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 208,925
FILING DATE: 20-NOV-1980
APPLICATION NUMBER: 449,447
FILING DATE: 12-DEC-1989
APPLICATION NUMBER: 860,893
FILING DATE: 08-MAY-1986
APPLICATION NUMBER: 208,925
FILING DATE: 20-NOV-1980
SEQ ID NO: 2
LENGTH: 212
5510472-2

Query Match 100.0%; Score 1071; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MMSFSTAFGVAASLGLVLPAPAPVPCEGDSKDYAAPHRQPLTSSERIDKQIRYI 60
DB 1 MMSFSTAFGVAASLGLVLPAPAPVPCEGDSKDYAAPHRQPLTSSERIDKQIRYI 60
QY 61 LDG1SALKRKETCNKSNMCESSKALAEENNINLPKMAEKDCGFCGPFNEETCIYK1ITGL 120
DB 61 LDG1SALKRKETCNKSNMCESSKALAEENNINLPKMAEKDCGFCGPFNEETCIYK1ITGL 120
QY 121 EFVEVLEYLQNRPFESSEORAVOMSTKVLIOFLQKKANLDAITTPPTTNASLITKIQ 180
DB 121 EFVEVLEYLQNRPFESSEORAVOMSTKVLIOFLQKKANLDAITTPPTTNASLITKIQ 180
QY 181 AONOMLQDMTHLLIRSFKEFLQSSLRALROM 212
DB 181 AONOMLQDMTHLLIRSFKEFLQSSLRALROM 212

RESULT 7
US-09-122-443-12
Sequence 12, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-12

Query Match 89.2%; Score 955; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.9e-97;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 25 AAPAPVPCEGDSKDYAAPHRQPLTSSERIDKQIRYILDDISALKRKETCNKSNMCESSKREA 84
DB 1 AAPAPVPCEGDSKDYAAPHRQPLTSSERIDKQIRYILDDISALKRKETCNKSNMCESSKREA 60
QY 85 LAENNLNPKMAEKDCGFCGPFNEETCIYK1ITGLLEFEVLEYLQNRPFESSEORAVQ 144
DB 61 LAENNLNPKMAEKDCGFCGPFNEETCIYK1ITGLLEFEVLEYLQNRPFESSEORAVQ 120
QY 145 MSTKVLIOFLQKKANLDAITTPPTTNASLITKLOAONOMLQDMTHLLIRSFKEFLQSS 204
DB 121 MSTKVLIOFLQKKANLDAITTPPTTNASLITKLOAONOMLQDMTHLLIRSFKEFLQSS 180
QY 205 SLRALROM 212
DB 181 SLRALROM 188

RESULT 8
US-07-632-070B-1
Sequence 1, Application US/07632070B
Patent No. 5264209
GENERAL INFORMATION:
APPLICANT: Mikayama, Toshihumi
APPLICANT: APPLICANT: Kadoya, Toshiko
APPLICANT: APPLICANT: Kakitani, Makoto
APPLICANT: APPLICANT: Inoue, Hideo
TITLE OF INVENTION: Modified hIL-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
STREET: Murray & Bicknell
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: NBI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/632,070B
FILING DATE: 19901221
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-32273
FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-22253
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-250460
FILING DATE: 21 SEPT 1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-07-632-070B-1

Query Match 87.6%; Score 938; DB 1; Length 185;

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Best Local Similarity 100.0%; Pred. No. 2,1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	28	APPPEDESDKDYAAHNRPLTSSERRIDKQIRYLLDQISALRRETCKNSMCESSKEALAE	87
Db	1	APPPEDESDKDYAAHNRPLTSSERRIDKQIRYLLDQISALRRETCKNSMCESSKEALAE	60
Qy	88	NNLNLPKAEKDCGFCGSGFNEFTCLVLTITGLLEFVYLEYLQNRFSSEBDQARAVOMST	147
Db	61	NNLNLPKAEKDCGFCGSGFNEFTCLVLTITGLLEFVYLEYLQNRFSSEBDQARAVOMST	120
Qy	148	KVLIQFLQKKAKNLDAITTPDPPTTNASLITKLOAQONQIMQDMTTHLILRSKREPLQSSLR	207
Db	121	KVLIQFLQKKAKNLDAITTPDPPTTNASLITKLOAQONQIMQDMTTHLILRSKREPLQSSLR	180
Qy	208	ALROM	212
Db	181	ALROM	185

RESULT 9
 US-07-918-181A-2
 Sequence 2, Application US/07918181A
 Patent No. 5338833
 GENERAL INFORMATION:
 APPLICANT: Fowlkes, Dana M.
 TITLE OF INVENTION: C-Terminal IL-6 Mutelins
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Imclone Systems Incorporated
 STREET: 180 Varick Street
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10014
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/918,181A
 FILING DATE: 23-JUL-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sheets, Eric J.
 REGISTRATION NUMBER: 30,326
 REFERENCE/DOCKET NUMBER: FOW-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-645-1405
 TELEFAX: 212-645-2054
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 195 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-918-181A-2

Query Match	87.6%	Score 938;	DB 1;	Length 185;
Best Local Similarity	100.0%	Pred. NO. 2.1e-95;		
Matches 185;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	28	APVPGEDSDVAAPPROPLTSSERIDKIRYLIGISALRKETCNKSNMCESSKEALAE	87
Db	1	APVPGEDSDVAAPPROPLTSSERIDKIRYLIGISALRKETCNKSNMCESSKEALAE	60
QY	88	NNNLPLPKAEKDCFGSGFNEETCLVKIITGLLEEVYLEYLNRFSSSEDAQAVQMST	147
Db	61	NNNLPLPKAEKDCFGSGFNEETCLVKIITGLLEEVYLEYLNRFSSSEDAQAVQMST	120
QY	148	KVLIIQELQKRAKNLDAITTPDPPTNNASLITLKIQAOONMLQDMTHLLIRSKKEFLQSSLR	207

Db 121 KVLQFLQKKAKNEDAITTPDPPTNSSLTKLQAQNGMDMTTHLIRSFKEFLQSSLR 180

QY	208	ALRQM	212
Db	181	ALRQM	185

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RESULT 10
US-08-231-575-2
: Sequence 2, Application US/08231575
: Patent No. 5565336
:
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incilone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/231.575
: FILING DATE: 22-Apr-1994
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/918.181
: FILING DATE: 23-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: FOM-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 195 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-231-575-2

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Query Match	87.6%	Score	938	DB 1	Length	185	
Best Local Similarity	100.0%	Pred. No.	2	1e-95			
Matches	185	Conservative	0	Mismatches	0	Indels	
					0	Gaps	
						0	
QY	28	APVPPGDSNDVAA	PHRPP	LTSSERIDQ	IRYILDG	ISALKREYCNKSNMCSSKXALAE	87
Db	1	APVPPGDSNDVAA	PHRPP	LTSSERIDQ	IRYILDG	ISALKREYCNKSNMCSSKXALAE	60
QY	88	NNLNLPMAARKDC	FCPSGFNEET	CLVK	IITG	LLFEFVYL	EVLYLQNRFPSSSEQARA
Db	61	NNLNLPMAARKDC	FCPSGFNEET	CLVK	IITG	LLFEFVYL	EVLYLQNRFPSSSEQARA
QY	148	KVLIQFLQKRAK	NLDATT	PPDTYNAS	LLTK	LOAONQWLODMTH	LLRSFKFEQSSLR
Db	121	KVLIQFLQKRAK	NLDATT	PPDTYNAS	LLTK	LOAONQWLODMTH	LLRSFKFEQSSLR
QY	208	ALROM	212				
Db	181	ALROM	185				
RESULT	11						

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US-08-246-427A-5
: Sequence 5, Application US/08246427A
: Patent No. 5641657
: GENERAL INFORMATION:
: APPLICANT: RUBEN, ET AL.
: TITLE OF INVENTION: Interleukin-6 Splice Variant
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
: ADDRESSER: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/246 427A
: FILING DATE: Submitted herewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/246,427
: FILING DATE: MAY 19, 1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: FERRARO, GREGORY D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
US-08-246-427A-5

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Query Match      87.6%; Score 938; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGDESKVAAPHROPITSSERIDKQIRYILDGIALRKETCKNSMCESSKEALAE 87
DB 1 AVPPGDESKVAAPHROPITSSERIDKQIRYILDGIALRKETCKNSMCESSKEALAE 60
QY 88 NNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQNFESSEEQARAVQKST 147
DB 61 NNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQNFESSEEQARAVQKST 120
QY 148 KVLIOFLQKKAKKNDAITTPDPTTNASLITKLOAQONQMDPTTHLILRSKEFLQSSLR 207
DB 121 KVLIOFLQKKAKKNDAITTPDPTTNASLITKLOAQONQMDPTTHLILRSKEFLQSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

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RESULT 12
: Sequence 5, Application US/08766620
: Patent No. 5958400
: GENERAL INFORMATION:
: APPLICANT: RUBEN, ET AL.
: TITLE OF INVENTION: Interleukin-6 Splice Variant

```

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: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
: ADDRESSER: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/766,620
: FILING DATE: December 12, 1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/246,427
: FILING DATE: MAY 19, 1994
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MULLINS, J.G.
: REGISTRATION NUMBER: 33,073
: REFERENCE/DOCKET NUMBER: 325800-593 (PF120)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
US-08-766-620-5

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Query Match      87.6%; Score 938; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGDESKVAAPHROPITSSERIDKQIRYILDGIALRKETCKNSMCESSKEALAE 87
DB 1 AVPPGDESKVAAPHROPITSSERIDKQIRYILDGIALRKETCKNSMCESSKEALAE 60
QY 88 NNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQNFESSEEQARAVQKST 147
DB 61 NNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQNFESSEEQARAVQKST 120
QY 148 KVLIOFLQKKAKKNDAITTPDPTTNASLITKLOAQONQMDPTTHLILRSKEFLQSSLR 207
DB 121 KVLIOFLQKKAKKNDAITTPDPTTNASLITKLOAQONQMDPTTHLILRSKEFLQSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

```

```

RESULT 13
: Sequence 2, Application PC/TUS9306928
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varlick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.

```

ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCY/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06928-2

Query Match 87.6%; Score 938; DB 5; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;

Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 87
DB 1 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 60
QY 88 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 147
DB 61 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 120
QY 148 KYLIOFLQKAKNLDATITPPPTTNASILTRKLOQONOMLODMTHILISFKFLOSSLR 207
DB 121 KYLIOFLQKAKNLDATITPPPTTNASILTRKLOQONOMLODMTHILISFKFLOSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

RESULT 14

Patent No. 5186931
APPLICANT: Kishimoto, Tadami; Hirano, Toshio; Akiyama, Yukio;
Okano, Akira; Matsui, Hiroshi; Takahara, Yoshiyuki
TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
MARROW TRANSPLANTATION
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/366,866
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 81,746
FILING DATE: 05-AUG-1987
SEQ ID NO: 2:
LENGTH: 185
5186931-2

Query Match 87.6%; Score 938; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 87
DB 1 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 60
QY 88 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 147
DB 61 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 120
QY 148 KYLIOFLQKAKNLDATITPPPTTNASILTRKLOQONOMLODMTHILISFKFLOSSLR 207
DB 121 KYLIOFLQKAKNLDATITPPPTTNASILTRKLOQONOMLODMTHILISFKFLOSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

RESULT 15

US-07-632-070B-2
Sequence 2, Application US/07632070B
Patent No. 5264209
GENERAL INFORMATION:
APPLICANT: Mikayama, Toshihumi
APPLICANT: APPLICANT: Kadoya, Toshiko
APPLICANT: APPLICANT: Kakitani, Makoto
APPLICANT: APPLICANT: Inoue, Hideo
TITLE OF INVENTION: Modified hIL-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
ADDRESSEE: Murray & Bicknell
STREET: 20 South Clark Street, Suite 2100
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: NEI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/632,070B
FILING DATE: 19901221
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-32273
FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-222353
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-250460
FILING DATE: 21 SEPT 1990
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 186
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
US-07-632-070B-2

Query Match 87.6%; Score 938; DB 1; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 87
DB 2 AVPPGDSKDVAAAPHROPPLTSSERIDKQIRYILDGISAARKETCKSNMCESSKEALAE 61
QY 88 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 147
DB 62 NNINLPKMAEKDGFOSGFNEETCLVKIITGLLEFEVYLEYLONRRESSSEGOARAVOMST 121

Fri Oct 5 10:02:12 2001

us-09-230-048-3.rai

Page 8

Qy	148	KVILQGLQKKAKNLDATTPPTNNASLITRKLOANOMLODMTHILIRSRKEFLQSLR	207
Qy	148	KVILQGLQKKAKNLDATTPPTNNASLITRKLOANOMLODMTHILIRSRKEFLQSLR	207
Db	122	KVILQGLQKKAKNLDATTPPTNNASLITRKLOANOMLODMTHILIRSRKEFLQSLR	181
Qy	208	ALROM	212
Qy	182	ALROM	186

Search completed: October 4, 2001, 19:10:32
Job time: 11.63 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:53 ; Search time 44.98 Seconds
 (Without alignments)
 359.026 Million cell updates/sec

Title: US-09-230-048-3
 Perfect score: 1071
 Sequence: 1 MNSFSTSGAPVAFSLGILL.....ILRSFKFLOSIRALROM 212

Scoring table: BIOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : PIR68:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1071	100.0	212	1 IVHUB2	interleukin-6 prec
2	660	61.6	208	2 T09216	interleukin-6 prec
3	659	61.5	212	2 I46590	interleukin 6 - pi
4	658	61.4	212	2 I46621	interleukin 6 -
5	567.5	53.0	207	2 I46084	interleukin 6 - ca
6	556	51.9	208	1 A56510	interleukin-6 prec
7	554	51.7	208	1 S29549	interleukin-6 - sh
8	435.5	40.7	211	2 A4247	interleukin-6 prec
9	420.5	39.3	211	1 ICMS6	interleukin-6 prec
10	123	11.5	201	2 A42247	myelomonocytic gro
11	99	9.2	208	2 A26496	granulocyte colony
12	99	9.2	1154	2 T15650	hypothetical prote
13	96	9.0	1290	2 A55094	chromosomal protei
14	94.5	8.8	1611	2 A84743	probable myosin he
15	94	8.8	253	2 C84644	probable ribonucle
16	94	8.8	600	2 T29879	hypothetical prote
17	94	8.8	1819	2 A11928	caag island protein
18	92.5	8.6	642	2 T39607	fork head protein
19	91.5	8.5	2269	2 T28677	thoxytry protein -
20	90	8.4	1281	2 JC5368	dynactin 1 - mouse
21	89	8.3	725	2 A47168	cardiac morphogene
22	87.5	8.2	539	2 F72288	methyl-accepting c
23	87.5	8.2	763	2 B86250	hypothetical prote
24	86.5	8.1	440	1 B70326	conserved hypothet
25	86.5	8.1	622	2 G36703	unknown protein, 3
26	86	8.0	1927	2 G64585	caag pathogenicity
27	84.5	7.9	1875	2 S38173	myosin-like protei
28	84	7.8	2319	2 A47004	coagulation factor
29	83.5	7.8	623	2 I46382	zpl precursor - mo

30	83	7.7	243	2 F64432	spore coat polysac
31	83	7.7	291	2 S48990	hypothetical prote
32	83	7.7	376	2 T32009	hypothetical prote
33	83	7.7	697	2 T07111	MAK binding filame
34	82.5	7.7	159	2 B81726	conserved hypothet
35	82.5	7.7	313	2 F72366	methionyl-tRNA for
36	82.5	7.7	809	2 S40460	ribosomal protein
37	82.5	7.7	1392	2 A43336	microtubule-vesicl
38	82.5	7.7	1427	2 S22695	restin - human
39	82	7.7	582	2 A41258	guanine nucleotide
40	82	7.7	689	2 T40364	hypothetical prote
41	82	7.7	1496	2 T19833	hypothetical prote
42	81.5	7.6	932	2 T30099	hypothetical prote
43	81.5	7.6	992	2 T46337	hypothetical prote
44	81.5	7.6	1846	2 T10670	hypothetical prote
45	81	7.6	622	2 S51972	SPC72 protein - ye

ALIGNMENTS

RESULT 1
 IVHUB2
 Interleukin-6 precursor (validated) - human
 N:Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
 on factor
 C:Species: Homo sapiens (man)
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
 C:Accession: A32648; A25692; A25956; A33515; A25801; A25921; I52193; I56003; A27601;
 R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
 EMBO J. 6, 2939-2945, 1987
 A:Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) 9
 A:Reference number: A32648; MUID:88082664
 A:Accession: A32648
 A:Molecule type: DNA
 A:Residues: 1-212 <FAS>
 A:Cross-references: GB:X04430; NID:929494; PIDN:CAA68278.1; PID:929495
 A:Note: the authors translated the codon CAG for residue 130 as Glu
 R:Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
 EMBO J. 5, 2529-2537, 1986
 A:Title: Structure and expression of cDNA and genes for human Interferon-beta-2, a dI
 A:Reference number: A91051; MUID:8705818
 A:Accession: A25692
 A:Molecule type: mRNA
 A:Residues: 1-212 <ZII>
 A:Cross-references: GB:X04430; NID:932673; PIDN:CAA28026.1; PID:932674
 R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwa
 I., T.; Kishimoto, T.
 Nature 324, 73-76, 1986
 A:Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
 A:Reference number: A93387; MUID:87065033
 A:Accession: A26966
 A:Molecule type: mRNA
 A:Residues: 1-212 <HIR>
 A:Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
 R:Tonouchi, M.; Miwa, K.; Karasuyama, H.; Matsui, H.
 Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
 A:Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
 A:Reference number: A33515; MUID:89391958
 A:Accession: A33515
 A:Molecule type: mRNA
 A:Residues: 1-212 <TON>
 A:Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
 R:Haegeman, G.; Content, J.; Voicakeert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
 Eur. J. Biochem. 159, 625-632, 1986
 A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
 A:Reference number: A25801; MUID:87004683
 A:Accession: A25801
 A:Molecule type: DNA; mRNA
 A:Residues: 1-212 <HAE>
 A:Cross-references: GB:X04403
 A:Experimental source: fibroblast
 R:May, L.T.; Helfgott, D.C.; Sengal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAV>
 A:Cross-references: GB:M4584; NID:g184628; PID:AA52728.1; PID:g306910
 R:Wong, G.G.; Witek-Glimott, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: 152193; MUID:89193317
 A:Accession: 152193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <WON>
 A:Cross-references: GB:M54894; NID:g186351; PID:AC41704.1; PID:g186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: 156003; MUID:8808768
 A:Accession: 156003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BNA>
 A:Cross-references: GB:M18403; NID:g184631; PID:AA52729.1; PID:g306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VAZ>
 R:Yamamoto, R.; Itoh, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <VAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Taketsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MUID:8792370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; An Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation f
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Pierino, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytokine in lymphocyte differentiation factor fo
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zaborskie, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human Interleukin-6.
 A:Reference number: A48419; MUID:91355644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAV2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A:Note: this 28-30K form contained both N-linked and O-linked carbohydrate: a 25K for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAV3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBI:63787)
 A:Note: this 23-25K form contained O-linked but not N-linked carbohydrate
 R:Orlitz, T.; Obedt, M.; Hasegawa, M.; Kibonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human Interleukin-6 pr
 A:Reference number: JX0305; MUID:94266765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human Interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, P.L.; Li, X.; Chong, P.; Ide, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human Interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 ibulin secretion). It therefore appears to function as an autoregulator of cell grow
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:116
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 F:1-37/Domains: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-37/Domains: signal sequence; status predicted <SIG>
 F:28-212/Product: Interleukin-6, long form #status experimental <MAV1>
 F:72-78/101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0% Score 1071; DB 1; Length 212;
 Best Local Similarity 100.0% Pred. No. 9 3e-80;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNSFSTSAFGVAFSLGLLVLPAAFPAPVPEQDSKDVAAPHRPPLTSSERIDKQIRYI	60
DB	1	MNSFSTSAFGVAFSLGLLVLPAAFPAPVPEQDSKDVAAPHRPPLTSSERIDKQIRYI	60
QY	61	LDGISALKEKCKNSNCKSSKALAEENNLNPKMAEKKGCFQSFNEETCIYITIGLL	120
DB	61	LDGISALKEKCKNSNCKSSKALAEENNLNPKMAEKKGCFQSFNEETCIYITIGLL	120
QY	121	EFVYVLELQNRPFSSREQARAVQNSTKVLQIQLQKAKNDATITPPTNASLTKLQ	180
DB	121	EFVYVLELQNRPFSSREQARAVQNSTKVLQIQLQKAKNDATITPPTNASLTKLQ	180
QY	181	AQNMQLDMTHLILRSFKFELQSSLRALROM	212
DB	181	AQNMQLDMTHLILRSFKFELQSSLRALROM	212

RESULT 2
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C:Date: 11-Jun-1999 #sequence
 C:Accession: T09216
 R:Swiderski, C.E.; Morohov, D.W.
 submitted to the EMBL data library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216

OY 181 AONQWLODM-TTHLILRSFKERLOSRLRALRQ 212
 DB 175 CSIRRVAAEAINNILLTRLEDEFLQALRAVRIR 207

RESULT 6
 A56610

Interleukin-6 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A56610; S22162

R:Proorganism: B.; Clusters: 1.; Cluster: Y.; Kettmann, R.; Burny, A.

DNA Seq. 2, 411-413, 1992

A:Title: Nucleotide sequence of bovine Interleukin-6 cDNA.

A:Reference number: A56610; MUID:93076003

A:Accession: A56610

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <PRO>

A:Cross-references: EMBL:X57317; NID:92193; PID:CAA40572.1; PID:92194

A:Experimental source: BLV Induced B cell-1 lymphosarcoma

A:Note: Sequence extracted from NCBI backbone (NCBIF:118917)

C:Superfamily: Interleukin-6

C:Keywords: cytokine

Query Match 51.7%; Score 556; DB 1; Length 208;

Best Local Similarity 53.8%; Pred. No. 5, 2e-38;

Matches 113; Conservative 35; Mismatches 38; Indels 4; Gaps 2;

OY 1 MNSFTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 60

DB 1 MNSFTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 60

OY 61 LDGISAIRKETCNKSNMCESSKALAEENNLNPKMAEKDGCQSGFNEETCLVITGL 120

DB 61 VDKISAIRKETCNKSNMCESSKALAEENNLNPKMAEKDGCQSGFNEETCLVITGL 120

OY 121 EFVYLEYLQNRSESEQARAVOMSTKYLQFLQKAKNLDAITTPDPTNASLIRQ 180

DB 121 EYQIYLDYLDQNEQGNQENVRDKRNIRLQIL--KQIADLITTP--PATNTDLLEKMQ 176

OY 181 AONQWLODM-TTHLILRSFKERLOSRLRALRQ 210

DB 177 SSNEVAKNAKILLIRNLLENFLQFSIRAIR 206

RESULT 7

S29349

Interleukin-6 - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S29349

R:Proorganism: B.

Submitted to the EMBL Data Library, October 1992

A:Reference number: S29349

A:Accession: S29349

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <EBS>

A:Cross-references: EMBL:X68723

C:Superfamily: Interleukin-6

Query Match 51.7%; Score 554; DB 1; Length 208;

Best Local Similarity 52.9%; Pred. No. 7, 5e-38;

Matches 111; Conservative 37; Mismatches 58; Indels 4; Gaps 2;

OY 1 MNSSTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 60

DB 1 MNSSTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 60

RESULT 8

A34247

Interleukin-6 precursor - rat

N:Alternate names: IL-6

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999

C:Accession: A34247

R:Northmann, W.; Bracklak, T.A.; Hattori, M.; Lee, F.; Fey, G.R.

J. Biol. Chem. 264, 16072-16082, 1989

A:Title: Structure of the rat Interleukin 6 gene and its expression in macrophage

A:Reference number: A34247; MUID:89380206

A:Accession: A34247

A:Status: preliminary

A:Molecule type: mRNA

OY 61 LDGISAIRKETCNKSNMCESSKALAEENNLNPKMAEKDGCQSGFNEETCLVITGL 120
 DB 61 VDKISAIRKETCNKSNMCESSKALAEENNLNPKMAEKDGCQSGFNEETCLVITGL 120

OY 121 EFVYLEYLQNRSESEQARAVOMSTKYLQFLQKAKNLDAITTPDPTNASLIRQ 180

DB 121 EYQIYLDYLDQNEQGNQENVRDKRNIRLQIL--KQIADLITTP--PATNTDLLEKMQ 176

OY 181 AONQWLODM-TTHLILRSFKERLOSRLRALRQ 210

DB 177 SSNEVAKNAKILLIRNLLENFLQFSIRAIR 206

RESULT 9

ICM56

Interleukin-6 precursor - mouse

N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepat

acytoma growth factor

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999

C:Accession: A30531; A27610; A30571; S01323; S12103; E44047; A26662; A40486; A60799;

R:Tanabe, O.; Akita, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.

J. Immunol. 141, 3875-3881, 1988

A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of poten

A:Reference number: A30531; MUID:89035525

A:Accession: A30531

A:Molecule type: DNA

A:Residues: 1-211 <TAN>

A:Cross-references: GB:M20572; NID:9198369; PID:AAA39302.1; PID:9387386

R:Van Snick, J.; Cayphas, S.; Szekora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.;

Eur. J. Immunol. 18, 193-197, 1988

A:Title: cDNA cloning of murine Interleukin-6; homology with human Interleukin 6.

Query Match 40.7%; Score 435.5; DB 2; Length 211;

Best Local Similarity 40.8%; Pred. No. 3, 1e-28;

Matches 87; Conservative 55; Mismatches 66; Indels 5; Gaps 4;

OY 1 MNSFTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 59

DB 1 MNSFTSAFPGVAFSGLLVLPAAPVPPGEDSKDVAAPHROPILTSSERIDKQIRY 57

OY 60 ILDCISAIRKETCNKSNMCESSKALAEENNLNPKMAEKDGCQSGFNEETCLVITGL 119

DB 58 VLREILMRKRELQNGSDCNSDNLSENNLKLPEIQNRDQGFQVQNGEILKICSL 117

OY 120 LEFVYLEYLQNRSESEQARAVOMSTKYLQFLQKAKNLDAITTPDPTNASLIRQ 178

DB 118 LEFVYLEYLQNRSESEQARAVOMSTKYLQFLQKAKNLDAITTPDPTNASLIRQ 177

OY 179 LQAQWLODM-TTHLILRSFKERLOSRLRALRQ 211

DB 178 LESQEWLRRRTIQLIKALDEFLKXTRMSTRQ 210


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Db      65 OLCRBEELQIVQDPRIHVLQV-APLDCHKRRQFOAEVCFQIRAGLHAYHDSLCAYLRLLPN 123
Oy      136 SEEDARAVOMSTKYLIOFLQKKAKN--LDAIT-----TPDDTTASLTLTLOQONQMLQ 187
Db      124 HTTIVERTLQDLAANLSSNICQMEDLDTVTLLPAEQKSPPTFS-----CPRQO 173
Oy      188 DMTHTHLLRSFKFEIAGSSIALAKOM 212
Db      174 QVGGFFILANFORLEFAYRALRHL 198

RESULT 11
A26496
granulocyte colony-stimulating factor precursor - mouse
N:Alternate names: G-CSF
C:Species: Mus musculus (house mouse)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 16-Jul-1999
C:Accession: A29536; A26496; S02493
R:Tauchiya, M.; Kaziro, Y.; Nagata, S.
Eur. J. Biochem. 165, 7-12, 1987
A:Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor
A:Reference number: A29536; MUID:87190474
A:Accession: A29536
A:Molecule type: DNA
A:Residues: 1-208 <TSU>
A:Cross-references: GB:X05402; NID:951059; PIDN:CAAZ8986.1; PID:951060
R:Tauchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986
A:Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimu
A:Reference number: A26496; MUID:87017003
A:Accession: A26496
A:Molecule type: mRNA
A:Residues: 1-208 <TS2>
A:Cross-references: GB:M13926; NID:9193451; PIDN:AAA37672.1; PID:9309248
R:Simpson, R.J.; Nicot, E.C.; Nicot, N.A.
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987
A:Title: Structural studies on the murine granulocyte colony-stimulating factor.
A:Reference number: S02493; MUID:88106598
A:Accession: S02493
A>Status: preliminary
A:Molecule type: protein
A:Residues: 31-34, 'X', 36-43; 48-51, 'X', 53-57, 'X', 60-71, 159-164, 'X', 166-176; 183-198, 'X', 20
C:Genetics:
A:Introns: 14/1; 71/3; 107/3; 156/3
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor; macrophage; monomer

Query Match          9.2%; Score 99; DB 2; Length 208;
Best Local Similarity 23.4%; Pred. No. 0.59;
Matches 36; Conservative 25; Mismatches 79; Indels 14; Gaps 3;

Oy      20 LVLAAPPAVPPGCEDSKVAAAPHRQPLTSSERIDKQIRYILIDGISALRKETCKSMNCE 79
Db      33 LVVYSAIPSPISIP-----LPRSLKLSLE----QVRKIQASGVLLHQLCATYKLC 79
Oy      80 SSKKALAEENLNLPKMAEKDGFQSGFNEETGLVKIITGLLEFVEYLEYLQNRRESSEEQ 139
Db      80 PEELVLLCHSLGCIPIK-ASLSGCCSSQAIQOTQCLSLHSGCLGIVQCLALSGISPALAPT 138
Oy      140 ARAVOMSTKYLIOFLQKKAKNLDATTPPTTNA 173
Db      139 LDLLQDLVAFNFTTIWQENLGVAPTVOPTOSA 172

RESULT 12
T15650
hypothetical protein C27A2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15650
R:Nhan, M.

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submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid C27A2.
A:Reference number: Z18382
A:Accession: T15650
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1154 <NHA>
A:Cross-references: EMBL:U58760; NID:91330384; PID:91330388; PIDN:AA00709.1; GSPDB:G
C:Experimental source: strain Bristol N2; clone C27A2
C:Genetics:
A:Gene: CESP:C27A2.1
A:Map position: 2
A:Introns: 31/2; 96/2; 140/3; 295/3; 405/1; 455/3; 533/3; 664/3; 714/3; 806/3; 899/3;

Query Match          9.2%; Score 99; DB 2; Length 1154;
Best Local Similarity 23.9%; Pred. No. 4.7;
Matches 49; Conservative 38; Mismatches 102; Indels 16; Gaps 6;

Oy      16 IGLILVPAAPPAVPPGCEDSKVAAAPHRQPLTSSERIDKQIRYILIDGISALRKETCKS 75
Db      603 LGFXYLVSNCFDAPAPLQPLCNVSGLNIPFGSD-VEKIAEVSQAIETQTRYSVELTA 661
Oy      76 NM-CSSKKEALAEENLNLPKMAEKDGFQSGFNEETGLVKITG--LLEFVEYLEYLQNR 132
Db      662 NLRONSKSRVANNTIQSGSATREANTWRDQFFKVPVAKRFDNSILEIQIKLAEIDIR 721
Oy      133 FESSEEDARAVOMSTKYLIOFLQKKAKNLDATTPPTTNASLTKLOAQONQMLQDHTT- 191
Db      722 SEQLREKKGALQKRDVLRQ-EDOMKRSKQVHTKTKTELSEMKLEALENEVDISAI 780
Oy      192 -----HLIRSFKEFLQSSLR 207
Db      781 EEEYANVEKKALLET-KKMLENSIR 804

RESULT 13
A55094
chromosomal protein XCAP-C - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C:Accession: A55094
R:Hirano, T.; Mitchison, T.J.
Cell 79, 449-458, 1994
A:Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensa
A:Reference number: A55094; MUID:95042742
A:Accession: A55094
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1290 <HIR>
A:Cross-references: GB:U13673; NID:9563811; PIDN:AAA64679.1; PID:9563812
C:Superfamily: chromosome segregation protein SKL1
C:Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match          9.0%; Score 96; DB 2; Length 1290;
Best Local Similarity 22.1%; Pred. No. 9.3;
Matches 44; Conservative 36; Mismatches 83; Indels 36; Gaps 8;

Oy      31 PGCEDSKVA-APHRQPLTSSERIDKQIRYILIDGISAL---RKETCNKSNKCESSKEAL- 85
Db      234 PKQGTFRHDEGMALRYLIDIIISERKKEPIQILCRPBLLENGEGLNKKVKEKALE 293
Oy      86 AENNLNLPKMAEKDGFQSGFNEETGLVKIITGLLEFVEYLEYLQNRRESSEEDQARAVOM 145
Db      294 GEKKKALEFLTVENETFKK--KNQLC-----QYIHDLOKRSRDEAKKEKIOE 340
Oy      146 STK-----VLIOFLQKKAKNLDATTPPTTNASLTKLOAQONQ-----LQDMTH 192
Db      341 DTKIISKSNLTLETKEKKKAL-----KDEKQKLNKTKTPEENREKFTOLDLDVDTR 395
Oy      193 LILRSFKFEIAGSSIALAKO 211

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Db 396 EKLKSKSVKKLOKOLK 414

RESULT 14

probable myosin heavy chain [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: A84743

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: A84743

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1611 <STO>

A:Cross-references: GB:AE002093; NID:96598338; PIDN:AAF18589.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2933240

A:Map position: 2

C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 8.8%; Score 94.5; DB 2; Length 1611;

Best Local Similarity 23.3%; Pred. No. 16;

Matches 40; Conservative 33; Mismatches 68; Indels 31; Gaps 5;

QY 34 EDSKDVAAFRHROPITSSERIDKQIYILDGIALRKETCNKSNMCESSKEALAEENNLNP 93

Db 917 ODAKTKLEKEVELTSCLEKQMELEQV-----KTQVEDLNSALNDMKLQL 966

QY 94 KMAEKGCQSGFNEETCIVKTIITGLFEFVYLYLQNRFFESSEQARAVOMSTKYLQIP 153

Db 967 -----GETQVTKSEE--TLKLSALQDMOLEFELAELEMTNDLA-AENEQLKDYSS 1017

QY 154 LQKAKNLDA-----ITTPDPTNASLITKIQAGQMWLQDMTHL 193

Db 1018 LQKKIDSDSKYETSKISEERVKQEPVLDQGVYIKLEAENCKLKALYSTL 1069

RESULT 15

C84644

probable ribonuclease large subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84644

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: C84644

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: GB:AE002093; NID:96623875; PIDN:AAF19216.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2925100

A:Map position: 2

Query Match 8.8%; Score 94; DB 2; Length 253;

Best Local Similarity 25.6%; Pred. No. 1.9;

Matches 46; Conservative 27; Mismatches 51; Indels 56; Gaps 8;

QY 35 DSKDVAAFRHROPITSSERIDKQIYILDGIALRKETCNKSNMCESSKEALAEENNLNP 94

Db 53 DSKTLKEKKEHEELYESLKDLSIGNAVVDIPR-----ELSAKMLAKKNTLNE 101

QY 95 MAEKDQCFQSGFNEETCIVKII--TGLEFEVYLE-----YLQNEFSESSEQARA 142

Db 102 ISH-----NSAMGLTKRVLDKMGVLLTFEAYLDQVGGDDPKRIKLSERFPS----- 145

QY 143 VOMSTVYLQF--LQKKAKNLDATTPDPTNASLITKL--QAQNMWLDQDMTHLILRSF 198

Db 146 -----IKFVYSKKAQDSLFPD-----VSGASIVAKYTRDRALKLEVLVEETGEDINRNF 192

Search completed: October 4, 2001, 19:09:55
Job time: 1256 sec

Fri Oct 5 10:02:13 2001

us-09-230-048-3.rpt

Page 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:12:32 ; Search time 27.34 Seconds
(without alignments) 265.624 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAFGPVAFSLGILL.....LILRSEKFEFLQSSLRALROM 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1071	100.0	212	1	IL6_HUMAN P05231 homo sapien
2	1033	96.5	212	1	IL6_MACPA P79341 macaca fasc
3	1032	96.4	212	1	IL6_MACMO P51494 macaca mola
4	1028	96.0	212	1	IL6_CERFO P46550 cercopithec
5	660	61.6	208	1	IL6_HORSE P26893 sus scrofa
6	658	61.4	212	1	IL6_PIG P26893 sus scrofa
7	657	61.3	209	1	IL6_PHOVI Q28819 phoca vitul
8	630	58.8	208	1	IL6_FELCA P41683 felis silve
9	627.5	58.6	207	1	IL6_CANPA P41323 canis fami
10	620.5	57.9	205	1	IL6_ORCOR Q28747 oreochinus orc
11	564	52.7	208	1	IL6_CAPHI Q28319 capra hircu
12	559	52.2	208	1	IL6_SHEEP P26892 ovis aries
13	556	51.9	208	1	IL6_BOVIN Q35736 marmota mon
14	472	44.1	207	1	IL6_MARMO Q35736 marmota mon
15	435.5	40.7	211	1	IL6_RAT P20607 rattus norv
16	420.5	39.3	211	1	IL6_MOUSE P08505 mus muscul
17	345	32.2	125	1	IL6_MUSVI P41693 mustela vis
18	123	11.5	201	1	MGE_CHICK P13854 gallus gall
19	99	9.2	208	1	CSEF_MOUSE P09920 mus muscul
20	96	9.0	1290	1	XCPC_XENLA P05032 xenopus lae
21	94	8.8	253	1	RNHL_ARATH Q95826 arabidopsis
22	93.5	8.7	539	1	MY53_HYDAT P33922 hydra atten
23	91.5	8.5	1280	1	DYNA_RAT P28023 rattus norv
24	90	8.4	1281	1	DYNA_MOUSE P08788 mus muscul
25	88.5	8.3	512	1	BNAI_HUMAN Q16515 homo sapien
26	88.5	8.3	512	1	BNAI_RAT Q62962 rattus norv
27	86.5	8.1	440	1	Y284_AOUAE Q66538 aquilifex aeo
28	84.5	7.9	1875	1	MUP1_YEAST Q02435 saccharomyc
29	84	7.8	2319	1	FAB_MOUSE Q06194 mus muscul
30	83	7.7	291	1	YH09_YEAST P38892 saccharomyc
31	83	7.7	1270	1	DYNA_HUMAN Q14203 homo sapien
32	82.5	7.7	313	1	FMT_THEMA Q9WY28 thermotoga
33	82.5	7.7	1427	1	REST_HUMAN P30622 homo sapien

34	82	7.7	592	1	CBP1_HUMAN P32455 homo sapien
35	81	7.6	622	1	YAE7_YEAST P38723 saccharomyc
36	81	7.6	1146	1	MYLC_MYCTU Q50585 mycobacteri
37	81	7.6	1244	1	GNRP_RAT P28818 rattus norv
38	81	7.6	2163	1	BRR2_YEAST P32639 saccharomyc
39	80.5	7.5	1679	1	Y109_YEAST P40457 saccharomyc
40	80	7.5	470	1	XNIF_XENLA P35617 xenopus lae
41	80	7.5	540	1	KNIC_CAEEL P46822 ceenothabdi
42	80	7.5	2209	1	Y166_HUMAN P50748 homo sapien
43	80	7.5	4540	1	DYHC_PASTE Q27171 paramacium
44	79.5	7.4	389	1	TOP2_PICGU Q01879 pichia guil
45	79.5	7.4	896	1	BOSS_DROME P22815 drosophilla

ALIGNMENTS

RESULT	ID	IL6_HUMAN	STANDARD	PRT	212 AA.
AC	P05231				
DT	13-AUG-1987	(Rel. 05, Created)			
DT	13-AUG-1987	(Rel. 05, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)				
DE	(INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).				
GN	IL6 OR IFN52.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RX	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE=87065033; PubMed=3491322.				
RA	Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,				
RA	Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunawake S.,				
RA	Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;				
RT	*Complementary DNA for a novel human Interleukin (BSF-2) that induces				
RT	B lymphocytes to produce immunoglobulin.*;				
RL	Nature 324:73-76(1986).				
RN	[2]				
RX	SEQUENCE FROM N.A.				
RX	MEDLINE=88082664; PubMed=3500852.				
RA	Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,				
RA	Nakai S., Kishimoto T.;				
RT	*Structure and expression of human B cell stimulatory factor-2				
RT	(BSF-2/IL-6) gene.*;				
RT	EMBO J. 6:2939-2945(1987).				
RN	[3]				
RX	SEQUENCE FROM N.A.				
RX	MEDLINE=87067433; PubMed=3538015;				
RA	May L.T., Hellgott D.C., Sehgal P.B.;				
RA	*Anti-beta-interferon antibodies inhibit the increased expression of				
RA	HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:				
RT	structural studies of the beta 2 interferon involved.*;				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).				
RN	[4]				
RX	SEQUENCE FROM N.A.				
RX	MEDLINE=87053818; PubMed=3023045;				
RA	Zilberstein A., Ruggieri R., Korn J.H., Revel M.;				
RA	*Structure and expression of cDNA and genes for human				
RA	interferon-beta-2, a distinct species inducible by growth-stimulatory				
RT	cytokines.*;				
RL	EMBO J. 5:2529-2537(1986).				
RN	[5]				
RX	SEQUENCE FROM N.A.				
RX	MEDLINE=88088768; PubMed=3320204;				
RA	Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,				
RA	Aarden L.A.;				
RT	*Molecular cloning and expression of hybridoma growth factor in				
RT	Escherichia coli.*;				
RL	J. Immunol. 139:4116-4121(1987).				
RN	[6]				

RP SEQUENCE FROM N.A.
 RX MEDLINE=89391958; PubMed=2789513;
 RA Todorouchi N., Miwa K., Karasuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human B2F-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Fibroblast;
 RC MEDLINE=87004683; PubMed=3758081;
 RA Haegeman G., Content J., Voicikert G., Derynck R., Tavernier J.,
 RA Fiers W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89193317; PubMed=3266463;
 RA Wong C., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Benfing Inst. Molec. Biol. 83:40-47(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93178270; PubMed=1291290;
 RA Chen O.Y.;
 RT "Stable and efficient expression of human Interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chin 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RX MEDLINE=88154445; PubMed=3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (NGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE=95154344; PubMed=7851440;
 RA Breton J., la Plante A., Bertolero F., Orsini G., Valsassina B.,
 RA Zlotoff R., de Filippis V., Polverino de Lauro P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RX MEDLINE=89286115; PubMed=2472117;
 RA Clogston C.L., Boone T.C., Grandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MUTAGENESIS.
 RX MEDLINE=91233808; PubMed=2037043;
 RA Luetjens C., Kruetgen A., Moeller C., Helinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96134845; PubMed=8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97303053; PubMed=9159484;

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RT "Solution structure of recombinant human Interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97224126; PubMed=9118960;
 RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of Interleukin 6: Implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBO J. 16:989-997(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOID AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC -----
 DR EMBL: X04430; CAA28026.1; -
 DR EMBL: M14584; AAA52728.1; -
 DR EMBL: X04602; CAA28268.1; -
 DR EMBL: Y00081; CAA68278.1; -
 DR EMBL: M18403; AAA52729.1; -
 DR EMBL: M29150; AAA59154.1; -
 DR EMBL: X04403; CAA27990.1; -
 DR EMBL: X04403; CAA27991.1; -
 DR EMBL: M54894; AAC41704.1; -
 DR EMBL: S56892; AAC13886.1; -
 DR EMBL: A09363; CAA00839.1; -
 DR PIR: A32648; IVH082.
 DR PIR: A25921; A25921.
 DR PDB: 1IL6; 04-FEB-98.
 DR PDB: 2IL6; 04-FEB-98.
 DR PDB: 1ALU; 03-JUN-98.
 DR MIM: 147620; -
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6.1.
 DR PRINTS: PR00433; IL6GSEMF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 212
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 73 73
 FT MUTAGEN 173 173
 FT MUTAGEN 185 185
 FT MUTAGEN 204 204
 FT MUTAGEN 210 210
 FT MUTAGEN 212 212
 FT SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;
 QY 1 MNSSTSAFQVAFVPSGLLVLPAPPAVPVPGESKDVAAAPHOPITSSSRIDKQRII 60
 QY 1 IINISSTSAFQVAFVPSGLLVLPAPPAVPVPGESKDVAAAPHOPITSSSRIDKQRII 60
 DB 1 MNSSTSAFQVAFVPSGLLVLPAPPAVPVPGESKDVAAAPHOPITSSSRIDKQRII 60
 QY 61 LDGISALRKETCKNSKNCSSSKKALAEKNLNLPKAAERDGGFGSGFNETCLVXITGLL 120
 QY 61 LDGISALRKETCKNSKNCSSSKKALAEKNLNLPKAAERDGGFGSGFNETCLVXITGLL 120
 DB 61 LDGISALRKETCKNSKNCSSSKKALAEKNLNLPKAAERDGGFGSGFNETCLVXITGLL 120

Query Match 100.0%; Score 1071; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4; 4e-80;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 EFEEVLEYLQNFESSEDOARAVOMSTKVLIOFLQKAKMLDAITTPPTTNASLITKIQ 180
DB 121 EFEEVLEYLQNFESSEDOARAVOMSTKVLIOFLQKAKMLDAITTPPTTNASLITKIQ 180
QY 181 AONOMLODMTTHLILRSKEFLQSSLRALROM 212
DB 181 AONOMLODMTTHLILRSKEFLQSSLRALROM 212

RESULT 2

IL6_MACFA STANDARD; PRT: 212 AA.
ID IL6_MACFA
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
GN INTERLEUKIN-6 PRECURSOR (IL-6).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL: AB000554; BAA19148.1; -
CC HSSP: P05231; 2116.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0189 CRC64;

Query Match 96.5%; Score 1033; DB 1; Length 212;
Best Local Similarity 96.7%; Pred. No. 5.3e-77;
Matches 205; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNSFSTASGPAVAFSLGLLVLPAPVPPGSDSKDVAAPHROPITSSERIDKIRYI 60
DB 1 MNSVSTASGPAVAFSLGLLVLPAPVPPGSDSKDVAAPHROPITSSERIDKIRYI 60
QY 61 LDGISALRKETCNKSNMCKSSKEALAEKNLNLPRMAEKDGCFOGSGFNEETCLVKIITGLL 120
DB 61 LDGISALRKETCNKSNMCKSSKEALAEKNLNLPRMAEKDGCFOGSGFNEETCLVKIITGLL 120
QY 121 EFEEVLEYLQNFESSEDOARAVOMSTKVLIOFLQKAKMLDAITTPPTTNASLITKIQ 180

DB 121 EFEEVLEYLQNFESSEDOARAVOMSTKVLIOFLQKAKMLDAITTPPTTNASLITKIQ 180
QY 181 AONOMLODMTTHLILRSKEFLQSSLRALROM 212
DB 181 AONOMLODMTTHLILRSKEFLQSSLRALROM 212

RESULT 3

IL6_MACMU STANDARD; PRT: 212 AA.
ID IL6_MACMU
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
GN INTERLEUKIN-6 PRECURSOR (IL-6).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL: L26028; AAA99978.1; -
CC HSSP: P05231; IL6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCAD CRC64;

Query Match 96.4%; Score 1032; DB 1; Length 212;
Best Local Similarity 96.2%; Pred. No. 6.4e-77;
Matches 204; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNSFSTASGPAVAFSLGLLVLPAPVPPGSDSKDVAAPHROPITSSERIDKIRYI 60
DB 1 MNSVSTASGPAVAFSLGLLVLPAPVPPGSDSKDVAAPHROPITSSERIDKIRYI 60
QY 61 LDGISALRKETCNKSNMCKSSKEALAEKNLNLPRMAEKDGCFOGSGFNEETCLVKIITGLL 120
DB 61 LDGISALRKETCNKSNMCKSSKEALAEKNLNLPRMAEKDGCFOGSGFNEETCLVKIITGLL 120

```

OY 121 EFVYLEYLONRFFSSSEQARAVOMSTKVLIQFLOKAKNLDATITPPPTNASLIRKQ 180
DB 121 EFVYLEYLONRFFSSSEQARAVOMSTKVLIQFLOKAKNLDATITPPPTNASLIRKQ 180
OY 181 AONQWLODMTHILRSFKEFIQSSLRALROM 212
DB 181 AONQWLODMTHILRSFKEFIQSSLRALROM 212

RESULT 4
IL6_CERTO STANDARD: PRT: 212 AA.
ID IL6_CERTO
AC P4650:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Cercopithecus.
OC NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUJ;
RX MEDLINE=96003435; Pubmed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Anagari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L26032; AAA99972.1; -
CC DR HSSP; P05231; IALU.
CC DR InterPro: IPR001716; -.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6CSFWMGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN6.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 POTENTIAL.
CC FT DISULFID 101 111 POTENTIAL.
CC FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CMC64;

Query Match 96.0%; Score 1028; DB 1; Length 212;
Best Local Similarity 95.8%; Pred. No. 1.4e-76;
Matches 203; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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DB 61 LDG1SALRKETCKNSKNCSSKCALAENNLNLPKMAEKDCGCSFGNEETCTVAKI FTGLL 120
OY 121 EFVYLEYLONRFFSSSEQARAVOMSTKVLIQFLOKAKNLDATITPPPTNASLIRKQ 180
DB 121 EFVYLEYLONRFFSSSEQARAVOMSTKVLIQFLOKAKNLDATITPPPTNASLIRKQ 180
OY 181 AONQWLODMTHILRSFKEFIQSSLRALROM 212
DB 181 AONQWLODMTHILRSFKEFIQSSLRALROM 212

RESULT 5
IL6_HORSE STANDARD: PRT: 208 AA.
ID IL6_HORSE
AC Q95181; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC Swiderski C.E., Horchov D.W.;
RA Submitted (DEC 1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RA Submitted (JUL 1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC Lai A.C.K.;
RA "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN 1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U64794; AAB87703.1; -
CC DR EMBL; AF005227; AAB62246.1; -
CC DR EMBL; AF041975; AAC04574.1; -
CC DR HSSP; P05231; IALU.
CC DR InterPro: IPR001716; -.
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6CSFWMGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN6.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 27 POTENTIAL.
CC FT CHAIN 28 208 INTERLEUKIN-6.
CC FT DISULFID 69 75 BY SIMILARITY.
CC FT DISULFID 98 108 BY SIMILARITY.
CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 4 5 US -> FF (IN REF. 1).
CC FT CONFLICT 8 8 T -> A (IN REF. 3).
CC FT CONFLICT 137 137 I -> V (IN REF. 2).
CC FT CONFLICT 205 205 V -> I (IN REF. 3).

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SQ SEQUENCENC 208 AA: 23325 MM: A62FAC234056BE66 CRC64:

Query Match 61.6%, Score 660; DB 1; length 208;
Best Local Similarity 61.3%, Pred. No. 8.8e-47;
Matches 130; Conservative 32; Mismatches 46; Indels 4; Gaps 2;

QY 1 MNSFSTSAFGPAFASIGLLILVLPAPAPVPPEGDSQDVAAPIHROPTSEERIDKOIRYI 60
DB 1 MNSLSTSTVTPAFAFSLGILLVMATFAFPPLPLGDEDTTNSGP---LLTTADKTKKHIXIYI 57
OY 61 LDOISSLKRETCRKSXMCSSCKEALAEENNLPMKAEKDCQFSGFNEETCLVXIIITGL 120
DB 58 LGRISLILKEMDCNNNSCKENSKREVAENNNLPMKAEKDCQFSGFNEETCLVXIIITGL 117
OY 121 EFPEVLEYLQNFPESSSEQARAVONSTVYLQIPLQKRAKNLDAITTPDPPTNASLTKLQ 180
DB 118 EFQIYIEYLQNEKKEKKEKNIKMTQSTVLVQIIMQKKKNE-VTTDPDPKASLLAKH 176
OY 161 AQONQMDMTLILHSKFEPLQSSLRALROM 212
DB 177 SQNEWMLKNTTTLILKSLSDPLQFSILRAVRIM 208

RESULT 6
IL6_PIG ID IL6_PIG STANDARD; PRT: 212 AA.
AC P26893;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91338547; PubMed=1873476;
RA Richards C., Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
RT expression of mRNA in synovial fibroblasts in vitro."
RL Cytokine 3:269-276(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92360284; PubMed=1497880;
RA Mathialagan N., Bixby J.A., Roberts M.R.;
RT "Expression of interleukin-6 in porcine, ovine, and bovine
RT preimplantation conceptuses."
RL Mol. Reprod. Dev. 32:324-330(1992).
CC CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC CC
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CC
CC EMBL; M86722; AAC37333.1; -
DR EMBL; M80258; AAC27127.1; -
DR HSSP; P05231; IALU.
DR InterPro; IPR001716; -
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.

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KW PROSITE:PS00254; INTERLEUKIN-6; 1.
FT CYTOKINE; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CONFLICT 30 30 G -> E (IN REF. 2).
SQ SEQUENCE 212 AA; 23880 MM; EF100ED030B6FDD0 CRC64;

Query Match 61.4%; Score 658; DB 1; Length 212;
Best Local Similarity 61.3%; Pred. No. 1,3e-46;
Matches 130; Conservative 32; Mismatches 50; Indels 0; Gaps 0;

OY 1 MNSFSTSAFSPVAFSLGLLLVLPAPAPVPVPGDSKDVAAAPRQPTSSERIDKQIRYI 60
Db 1 MNSLSTSAFSPVAFSLGLLLVMAFAFPPIPGSLIEDAGDATSKMLTSPDKTEELIKYI 60

OY 61 LDGTSALRKETCKSNMCESSSEALAEENMLPMAEKDCFGSGFNEETCLVYKITGLL 120
Db 61 LGSIAARRKCKMCKEYKCNSEKVEYLAENMLPMAKARDCCFGSGFNEETCLVYKITGLV 120

OY 121 EFPEYLEYLYQNRRESSEBQARAVQNSTVYLIOFLQKRAKMLNDITTPDPTNASTLTQLQ 180
Db 121 EFQYLDLYDLQKESNKKGNVEAVQISTALLQTLRQKGNKPDKATTPNPTTNGLLDKQ 180

OY 181 AONQMDMTHTLLILASFKEPLQSSLRALROM 212
Db 181 SONEMKMKRTIILILSLPDLQSLRAIRIM 212

RESULT 7
IL6_PROV1 IL6_PROV1 STANDARD: PRT: 209 AA.
AC 028819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6-PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plinipedia; Phocidae; Phoca.
CX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96163018; PubMed-8575817;
RA King D.P., Schenkel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Scott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:1190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL: L46802; AAB01430.1; -
DR HSSP: P05231; 21L6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U1234: AAA83030.1; -
CC HSP: P05231; 2116;
CC InterPro: IPR001716; -
CC Pfam: PF00489; IL6; 1;
CC PRINTS: PR00433; IL6CSEKGF;
CC PRINTS: PR00434; INTERLEUKIN6;
CC PROSITE: PS00254; INTERLEUKIN6; 1;
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 207
CC CHAIN ? 207 INTERLEUKIN-6.
CC FT DISULFID 67 73 BY SIMILARITY.
CC FT DISULFID 96 106 BY SIMILARITY.
CC FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 207 AA: 22945 MW: 45540154EABCP50 CRC64;

Query Match 58.6%; Score 627.5; DB 1; Length 207;
Best Local Similarity 59.0%; Pred. No. 3.7e-44;
Matches 125; Conservative 34; Mismatches 48; Indels 5; Gaps 1;

QY 1 MNSFSTSAFGVAFSLGLLVPAAPAPVPGEDSKDVAAPRQPTTSERIDKQIRTI 60
DB 1 MNSLSTST---AFSLGLLVATAFPVPGPLADSDKDDTSLSPLTSANKEBELIKYI 55
QY 61 LDGIALRKETCNKSNMCESSKEALAEENNLPRMAKDCGFGSGNEETCLVKITGL 120
DB 56 LKISALRKEMCDKRNKEDSKALAEENNLPRLEKSDCGFGSGNOCETCLRTITGLV 115
QY 121 EREYVLEYLQNFESSEQARAVQSTKVLQFLQKAKNLDAITPPDPTNASLTKIQ 180
DB 116 EYQHLNITLQNNYEEDKENVKSVHSTRKILVOMKSKVKNQDEVTTPDPTNASLQAIQ 175
QY 181 AQNMLODWTHTLIRSFKEFLOSSLRALROM 212
DB 176 SQDECKHTHTLIRSLDEFLQFLSLAVRIRM 207

RESULT 10
IL6_ORCOR
ID IL6_ORCOR STANDARD; PRT: 205 AA.
AC Q28747;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orcinus orca (killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96163018; PubMed=8575617;
RA King D.P., Schrenzel M.D., McKnight M.L., Reldarson T.H., Hanni K.D.,
RA Scott J.L., Perlick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RT Immunogenetics 43:190-195(1996)
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOGA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY
CC -----
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CC -----
CC EMBL: U46803; AB01429.1; -
CC HSP: P05231; IL6.
CC InterPro: IPR001716; -
CC Pfam: PF00489; IL6; 1;
CC PROSITE: PS00254; INTERLEUKIN6; 1;
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 21
CC CHAIN ? 21 BY SIMILARITY.
CC FT DISULFID 64 70 BY SIMILARITY.
CC FT DISULFID 93 103 BY SIMILARITY.
CC FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 205 AA: 23266 MW: 6308F3A457960832 CRC64;

Query Match 57.9%; Score 620.5; DB 1; Length 205;
Best Local Similarity 61.8%; Pred. No. 1.4e-43;
Matches 123; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 13 AFSGLGLLVPAAPAPVPGEDSKDVAAPRQPTTSERIDKQIRTIIDGIALRKETC 72
DB 5 AFSGLGLLVATAFPVPGPLADSDKDDTSLSPLTSANKEBELIKYI LKISAMKRENC 64
QY 73 NKNMCESSKEALAEENNLPRMAKDCGFGSGNEETCLVKITGLEREYVLEYLQNR 132
DB 65 EKYDKCENSKALAEENNLPRMAKDCGFGSGNOCETCLRTITGLERQIYLDVQNE 124
QY 133 FESSEQARAVQSTKVLQFLQKAKNLDAITPPDPTNASLTKLAQR-OMLODPT 191
DB 125 YEDDKATIAVAQISSKALQILRKQVKNPDVTPDPTNASLNNLOSONDMKMTKI 184
QY 192 HTLIRSFKEFLOSSLRALR 210
DB 185 ILIRSLDENFLQFLSLAIR 203

RESULT 11
IL6_CAPHI
ID IL6_CAPHI STANDARD; PRT: 208 AA.
AC Q28319;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97392354; PubMed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells.";
RT Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOGA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D86569; RAAL3118.1; -
CC      DR      HSSP: P05231; 21L6.
CC      DR      InterPro: IPR001716; -
CC      DR      Pfam: PF00489; IL6; 1.
CC      DR      PRINTS: PR00433; IL6CSFNGF.
CC      DR      PRINTS: PR00434; INTERLEUKIN6.
CC      DR      PROSITE: PS00254; INTERLEUKIN6; 1.
CC      CYCLOKING: Glycoprotein; Growth factor; Signal.
CC      FT      SIGNAL      1      29      BY SIMILARITY.
CC      FT      CHAIN      30      208      INTERLEUKIN-6.
CC      FT      DISULFID      72      78      BY SIMILARITY.
CC      FT      DISULFID      101      111      BY SIMILARITY.
CC      FT      CARBOHYD      38      38      N-LINKED (GLCNAC...) (POTENTIAL).
CC      FT      SEQUENCE      208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;
CC
Query Match      52.7%; Score 564; DB 1; Length 208;
Best Local Similarity 53.3%; Pred. No. 5,30-39;
Matches 112; Conservative 37; Mismatches 57; Indels 4; Gaps 2;

OY      1 MNSSTSAFGVAFSLGLLVLPAAPAPVPPGDSKDVAAPHROPLTSSRIDKQIRYI 60
DB      1 MNSLFTSAFSLAVSLGLLVLMTSAPPTGPGLGEDPKNDTTPSRLTLTPKTEALIKHI 60
OY      61 LDGISALAKKECKNSNMCKSSKEALAEENNLIPKMAEKDCGSGFNEETLVKIFGL 120
DB      61 VDKISALRKEICEKNDCKNSKTELAENKLIKPKMEKCGSGSFNAICLLITTAGLL 120
OY      121 EFEVYLELONREFFSESEDAVAVOMSTKVLIQLOKAKNLDATTPPTNNAISLTKLQ 180
DB      121 EYOIYLDPLONREFGNOETVMELOSSIRTLQILKRIAGL--ITT--PATHTMLEKMO 176
OY      177 SSNEVAKAKYIIILRSLENFLQPSRAIR 206
DB
RESULT 12
ID IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E.; Barclay G.J.; Ashman K.; Meusen E.N.T.; Brandon M.R.;
RA Nash A.D.;
RT "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA."
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ederhimi B.;
RL Submitted (OCT-1992) to the EMBL/Genbank/DBJ databases
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

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CC      FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC      OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC      PLASMACTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC      HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC      -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC      -----
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X62501; CAA44363.1; -
CC      DR      EMBL: X68723; CAA48662.1; -
CC      DR      EMBL: A19159; CAA01443.1; -
CC      DR      PIR: S29549; S29549.
CC      DR      HSSP: P05231; 21L6.
CC      DR      InterPro: IPR001716; -
CC      DR      Pfam: PF00489; IL6; 1.
CC      DR      PRINTS: PR00433; IL6CSFNGF.
CC      DR      PRINTS: PR00434; INTERLEUKIN6.
CC      DR      PROSITE: PS00254; INTERLEUKIN6; 1.
CC      CYCLOKING: Glycoprotein; Growth factor; Signal.
CC      FT      SIGNAL      1      29      BY SIMILARITY.
CC      FT      CHAIN      30      208      INTERLEUKIN-6.
CC      FT      DISULFID      72      78      BY SIMILARITY.
CC      FT      DISULFID      101      111      BY SIMILARITY.
CC      FT      CARBOHYD      38      38      N-LINKED (GLCNAC...) (POTENTIAL).
CC      FT      CONFLICT      4      4      L -> R (IN REF. 2).
CC      FT      CONFLICT      110      110      I -> V (IN REF. 2).
CC      FT      CONFLICT      171      171      M -> L (IN REF. 2).
CC      FT      CONFLICT      201      201      S -> R (IN REF. 2).
CC      FT      SEQUENCE      208 AA; 23446 MW; EBC96613E3230A0 CRC64;
CC
Query Match      52.2%; Score 559; DB 1; Length 208;
Best Local Similarity 52.9%; Pred. No. 1,3e-38;
Matches 111; Conservative 38; Mismatches 57; Indels 4; Gaps 2;

OY      1 MNSSTSAFGVAFSLGLLVLPAAPAPVPPGDSKDVAAPHROPLTSSRIDKQIRYI 60
DB      1 MNSLFTSAFSLAVSLGLLVLMTSAPPTGPGLGEDPKNDTTPSRLTLTPKTEALIKHI 60
OY      61 LDGISALAKKECKNSNMCKSSKEALAEENNLIPKMAEKDCGSGFNEETLVKIFGL 120
DB      61 VDKISALRKEICEKNDCKNSKTELAENKLIKPKMEKCGSGSFNAICLLITTAGLL 120
OY      121 EFEVYLELONREFFSESEDAVAVOMSTKVLIQLOKAKNLDATTPPTNNAISLTKLQ 180
DB      121 EYOIYLDPLONREFGNOETVMELOSSIRTLQILKRIAGL--ITT--PATHTMLEKMO 176
OY      177 SSNEVAKAKYIIILRSLENFLQPSRAIR 206
DB
RESULT 13
ID IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN:
RX MEDLINE-93076003; PubMed-1446077;
RA Droganas L., Cludis I., Cleuter Y., Kettmann R., Burny A.:
RT Nucleotide sequence of bovine Interleukin-6 cDNA.;
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
CC EMBL: X57317; CAA40572.1;
CC PIR: S22162; S22162.
CC DR HSSP: P05231; 21I6.
CC DR InterPro: IPR001716;
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PRO0433; IL6GCSFNGF.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 208
CC FT DISULFID 72 78
CC FT DISULFID 101 111
CC FT CARBOHYD 38 38
CC FT DISULFID 101 111
CC FT CARBOHYD 38 38
CC SEQUENCE 208 AA; 23758 MW; A0F00B9BA2EC341 CRC64;

Query Match 51.9%; Score 556; DB 1; Length 208;
Best Local Similarity 53.8%; Pred. No. 2,3e-38;
Matches 113; Conservative 35; Mismatches 58; Indels 4; Gaps 2;

OY 1 MNSFSTAGPAPFSLGLVLPAPAPVPDGDSDVAAPHROPLTSSERIDKQIRY 60
DB 1 MNSRFTSATTPAVALSGLLVVTSFPTPGLEGEDFNDDTTPGRLITPEKIALIKRM 60
OY 61 LGISALRKETCNKSNMCCSEKALAEENNLNLPMAEKDGCFOSGNEETCLVKITGLL 120
DB 61 VKISAMRKEICEKNDCESEKELAEKLNLPKMEKDCGFCOSGNOAICLIRTAGLL 120
OY 121 EFVYLEYVKNFESSEFOARVQSTKVLIOFLQKAKNLDAITTPDTNASILTKIO 180
DB 121 EYVITLDYIYQNYEGNÖGENDKRNIRITLIQIL--KQIADLIT--PATINDLEKMO 176
OY 181 AQONQLDMTHLLIRSEKFIQSSLRALR 210
DB 177 SSNEWYKNAKILILRLNLENLQESLRAIR 206

RESULT 14
IL6_MARMO STANDARD; PRT; 207 AA.
AC 035736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;

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RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Periphereal blood;
RX MEDLINE-98139533; PubMed-9472070;
RA Lohenguel B., Lu M., Rogendorf M.;
RT Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6.*;
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y14139; CAA74571.1;
CC DR InterPro: IPR001716;
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PRO0433; IL6GCSFNGF.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 207
CC FT DISULFID 65 71
CC FT DISULFID 94 104
CC FT DISULFID 94 104
CC SEQUENCE 207 AA; 23770 MW; F30D19F86AD6A600 CRC64;

Query Match 44.1%; Score 472; DB 1; Length 207;
Best Local Similarity 46.7%; Pred. No. 1,5e-31;
Matches 93; Conservative 41; Mismatches 63; Indels 2; Gaps 1;

OY 15 SLGLLVATAPAPFAPVPDGDSDVAAPHROPLTSSERIDKQIRYILDGSAIRKETCK 74
DB 8 SLGLLVATAPAPFAPFASLOREDGNSVTRNKPTRASCKTRQSLYLKREYFENRKE/CNN 67
OY 75 SNMCCSEKALAEENNLNLPKMAEKDGCFOSGNEETCLVKITGLLEFVYLEYLONRRE 134
DB 68 DEICIRSHVAAGSENNLNLPKMEKDCGFCOTGYNDDCLVITSGLEFYLYLIRNKFO 127
OY 135 SSEQARA--VQMSKVLIOFLQKAKNLDAITTPDTNASILTKIOAQONQLDMTH 192
DB 128 EGNRRRAEHVSSKALIEILQEVKDPKIVPSPANINLAKESQNDQKQVYMO 187
OY 193 LIRSEKFIQSSLRALRQ 211
DB 188 LILSNFEDFLQFTLRAVRK 206

RESULT 15
IL6_RAT STANDARD; PRT; 211 AA.
AC P20607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.

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RX MEDLINE-89380206: PubMed-2789217;
RA Northmann W., Bracklax T.A., Hettlori M., Lee F., Fey G.H.;
RT "Structure of the rat interleukin 6 gene and its expression in
RT macrophage-derived cells.";
RL J. Biol. Chem. 264:16072-16082(1989).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IC-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch)
CC -----
DR EMBL: M26744; AAA77659.1; -
DR EMBL: M26745; AAA41430.1; -
DR PIR: A34247; A34247.
DR HSSP: P05231; 1AL0.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6GCSFMGF.
DR PRINTS: PRO0434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Growth factor; Glycoprotein; Signal.
KW CHAIN
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

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Query Match 40.7%; Score 435.5; DH 1; Length 211;
Best Local Similarity 40.8%; Pred. No. 14e-28;
Matches 87; Conservative 55; Mismatches 66; Indels 5; Gaps 4;

QY 1 MNSESTSAQVAFSLGLLVLPAFP-APVPEGDSKDVAPHRQPLTSSERIDQIRY 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MKFLSARDFQVAF-LGLMLITAFPTSOVRKGDPTEDVT--HNRPVYTTTSOVGLITY 57

QY 60 ILDGSLARKETCKSNMCKSSKALAEENLNPKMAEKDGCFOGSEFNEICLVKITGL 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 58 VLRIETLEKKKELCGNSDCKNSDLSNNLKLPEIORNDGCFQGYNOETCLKICSGC 117

QY 120 LEFEVYLYEQNR-ESSEDOARAYQSTKVLIOFLQKKAKMDAITTPDPTNNSLTLTK 178
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 118 LEFRYYLEFVNNQDNKKDKARVIOSTETLVHIFKQEKIDSKYKIVLPTPSNALLMEK 177

QY 179 LOAONOMIQDMTHLILRSFKEFIOSSLRALAQ 211
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 LRSQKRWLRTTIOILIKALEERFLKVTMRSTRO 210

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Search completed: October 4, 2001, 19:12:34
Job time: 269 sec


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DB 61 LDG1SALRKETCNKSNKCESSKEALAEENNINLPKMAEKKGCCGOSFNEETCLVYITIGLL 120
OY 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPPTTNASLTKLQ 180
DB 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPPTTNASLTKLQ 180
OY 181 AONQWLODMTTHILRSFKFELQSSLRAL 209
DB 181 AONQWLODMTTHILRSFKFELQSSLRAL 209

RESULT 2
O97TH3 PRELIMINARY: PRT: 209 AA.
AC O97TH3
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Gratiata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarrojo M.E.;
RT "Aotus lemurinus gene for IL-6."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF097323; AAF21298.1;
DR HSSP; P05231; 1A/U.
DR InterPro; IPR003573;
DR InterPro; IPR003574;
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6CSPMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT NON_TER 209
FT SEQUENCE 209 AA; 23115 MW; A0A3DFA4BF560CC CnC64;

Query Match 86.3%; Score 924; DB 6; Length 209;
Best Local Similarity 89.0%; Pred. No. 4.3e-75;
Matches 186; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 1 MNSFSTAFGCVAFSLGILVLPAPAPVPCEDSKDYAAPHRQPLTSSRIDKQIRYI 60
DB 1 MNSFSTAFGCVAFSLGILVLPAPAPVPCEDSKDYAAPHRQPLTSSRIDKQIRYI 60
OY 61 LDG1SALRKETCNKSNKCESSKEALAEENNINLPKMAEKKGCCGOSFNEETCLVYITIGLL 120
DB 61 LDG1SALRKETCNKSNKCESSKEALAEENNINLPKMAEKKGCCGOSFNEETCLVYITIGLL 120
OY 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPPTTNASLTKLQ 180
DB 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPPTTNASLTKLQ 180
OY 181 AONQWLODMTTHILRSFKFELQSSLRAL 209
DB 181 AONQWLODMTTHILRSFKFELQSSLRAL 209

RESULT 3
O97TH4 PRELIMINARY: PRT: 175 AA.
AC O97TH4
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)

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DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nigricaps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Gratiata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarrojo M.E.;
RT "Aotus nigricaps gene for IL-6."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF097322; AAF21297.1;
DR HSSP; P05231; 1A/U.
DR InterPro; IPR002069;
DR InterPro; IPR003573;
DR InterPro; IPR003574;
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6CSPMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PRODOM; PD002435;
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CnC64;

Query Match 69.3%; Score 742; DB 6; Length 175;
Best Local Similarity 87.0%; Pred. No. 6.6e-59;
Matches 148; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 1 MNSFSTAFGCVAFSLGILVLPAPAPVPCEDSKDYAAPHRQPLTSSRIDKQIRYI 60
DB 1 MNSFSTAFGCVAFSLGILVLPAPAPVPCEDSKDYAAPHRQPLTSSRIDKQIRYI 60
OY 61 LDG1SALRKETCNKSNKCESSKEALAEENNINLPKMAEKKGCCGOSFNEETCLVYITIGLL 120
DB 61 LDG1SALRKETCNKSNKCESSKEALAEENNINLPKMAEKKGCCGOSFNEETCLVYITIGLL 120
OY 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPDP 169
DB 121 EFVYLEYLONRFSSSEQARAVQSTKVLIOFLQKAKNLDATTPDP 169

RESULT 4
O97535 PRELIMINARY: PRT: 160 AA.
AC O97535
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Gratiata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarrojo M.E., Murillo L.A.;
RA "Identification, cloning and sequencing of different Interleukin genes
in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF014505; AAD01531.1;
DR HSSP; P05231; IL6.
DR InterPro; IPR003573;
DR InterPro; IPR003574;
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6CSPMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1

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Fri Oct 5 10:02:14 2001

SQ SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

Query Match

Best Local Similarity 62.08; Score 664; DB 6; Length 160;
Matches 131; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 DB 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 OY 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 DB 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 OY 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148
 DB 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148

RESULT 5

Q9MYZ7 PRELIMINARY; PRT; 207 AA.

AC Q9MYZ7
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Youn H.-Y., Shin I.-S.;
 RT "Canine IL-6 mRNA."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275796; AAF86275.1;
 DR InterPro; IPR003573;
 DR InterPro; IPR003574;
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GSGFNGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SMART; SM00126; IL6; 1.
 SQ SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

Query Match 60.18; Score 643.5; DB 6; Length 207;

Best Local Similarity 59.98; Pred. No. 5.2e-50;

Matches 127; Conservative 33; Mismatches 47; Indels 5; Gaps 1;

OY 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 DB 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 OY 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 DB 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 OY 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148
 DB 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148

RESULT 6
 Q9MYZ7 PRELIMINARY; PRT; 208 AA.
 ID Q9MYZ7

AC Q9MYZ7

DT 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)

DE INTERLEUKIN 6 PRECURSOR.

OC Delphinapterus leucas (Beluga whale).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;

OC Monodonta; Delphinapterus.

OX NCBI_TaxID=9749;

RN [1]

RP SEQUENCE FROM N.A.

RA St-Laurent G., De Guise S., Fournier M., Archambault D.;

RT "Molecular cloning and phylogenetic analysis of beluga whale

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF076643; AAD42929.1;

DR HSSP; P05231; IAU

DR InterPro; IPR003573;

DR InterPro; IPR003574;

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GSGFNGF.

DR PRINTS; PR00434; INTERLEUKIN6.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

SQ SEQUENCE 208 AA; 23456 MW; 81C85CE80389C4 CRC64;

Query Match 58.58; Score 626; DB 6; Length 208;

Best Local Similarity 60.28; Pred. No. 1.9e-48;

Matches 127; Conservative 28; Mismatches 50; Indels 6; Gaps 2;

OY 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 DB 1 NNSFSTSAFGVAVASLGLLVLPAPAPVPYPCGDSKDVAAPRQPLTSSERIDKQIRYI 60
 OY 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 DB 61 LDGIALRKRETCNKSNNCESSKEALAEENNINLPMAEKDGCFOSGFNEETCLVKIITGLL 120
 OY 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148
 DB 121 EFVYLEYLQNRFFESSEQAAVOMSTK 148

RESULT 7
 Q28403 PRELIMINARY; PRT; 207 AA.
 AC Q28403
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Euhadra lutris (Sea otter).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Euhadra.
 OX NCBI_TaxID=34882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT Southern sea otter (Euhadra lutris nelesi)."
 RL Immunogenetics 43:190-195(1996).
 DR EMBL; I46804; AAB01428.1;
 DR HSSP; P05231; IL6.

DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00469; IL6; 1
 DR PRINTS: PR00433; IL6CSFNGF
 DR PRINTS: PR00434; INTERLEUKIN6
 DR PROSITE: PS00254; INTERLEUKIN_6; 1
 DR SMART: SM00126; IL6; 1
 FT NON_TER 1
 SQ SEQUENCE 207 AA: 23527 MW: 7298E0CD91136D8B CXC64;

Query Match 56.38; Score 603; DB 6; Length 207;
 Best Local Similarity 57.78; Pred. No. 2,2e-46;
 Matches 120; Conservative 37; Mismatches 49; Indels 2; Gaps 1;

QY 5 STSAFCVAFSLGLLVLPAPFAPVPFGEDSKDVAAPHRQPLTSSERIDKQIRYLIDGI 64
 DB 2 STSAFSPVAFSLGLLVNATFAFPTPGPLGDSKDDATSNRPPLTSADKMEQIFIKIGKI 61
 QY 65 SALAKRECNKSNKCESEKALAEENNLNPKMAEKDCGFCGSGNEETCLVKITITGLEFEV 124
 DB 62 SALAKRECNKSNKCESEKALAEENNLNPKMAEKDCGFCGSGNEETCLVKITITGLEFEV 121
 QY 125 YLEVLQNRFFESSEQARAVQSTKVLQIQLQKRNKLDATTPPTNASLITKLAQONQ 184
 DB 122 HLKYLESNYEGNKNDAHSYISTKILLQTL--RPMNQLEVTTPPTDASLQALFSGQDK 179
 QY 185 WLODMTHLILRSKFELQSSLRALRQ 212
 DB 180 WLKHTTHILRLRLEDFQPSLRNIRIM 207

RESULT 8
 Q9JHH3 PRELIMINARY; PRT: 207 AA.
 ID Q9JHH3
 AC Q9JHH3
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmosa monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OC NCBI_TaxID=9995;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA LI D.H., Cullen J.M.;
 RT "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis.";
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RC LI D.H., Cullen J.M.;
 RT "Gene Structure of the Woodchuck Interleukin-6.";
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF012508; AAF34861.1; -
 DR EMBL: AF122896; AAF28873.1; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00469; IL6; 1.
 DR PRINTS: PR00433; IL6CSFNGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA: 23645 MW: AD2F46E450E13470 CRC64;

Query Match 43.98; Score 470; DB 11; Length 207;
 Best Local Similarity 46.78; Pred. No. 1.7e-34;
 Matches 93; Conservative 40; Mismatches 64; Indels 2; Gaps 1;

QY 15 SLGLILVLPAPFAPVPFGEDSKDVAAPHRQPLTSSERIDKQIRYLIDGISALAKRECNK 74
 DB 8 SLGLILVLPAPFAPFASLQREDGNSVTRNKPTRASSGKAGQISLYLIEVEEMKRELCN 67
 QY 75 SNKCESEKALAEENNLNPKMAEKDCGFCGSGNEETCLVKITITGLEFEVLEYLQNRFE 134
 DB 68 DETCIKSHVAVSENNLNPKYTEKDCGFCGVRNDCVLRITSGLEQYVLRIRKQFQ 127
 QY 135 SSEQARA--VQNSTKVLQIQLQKRNKLDATTPPTNASLITKLAQONQMDMTTH 192
 DB 128 EGNMNDRAEHVQSSKALIEILQKVDPKRTVFPSPANINLAKLESQNDQKVMTMQ 187
 QY 193 LILRSKFELQSSLRALRQ 211
 DB 188 LILRSKFELQFTLRAVRK 206

RESULT 9
 Q9MZRI PRELIMINARY; PRT: 241 AA.
 ID Q9MZRI
 AC Q9MZRI
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN, LYMPH NODE;
 RA MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the European rabbit (Oryctolagus cuniculus).";
 RL CytoKine 12:555-565(2000).
 DR EMBL: AF169176; AAF86660.1; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00469; IL6; 1.
 DR PRINTS: PR00433; IL6CSFNGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN.1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 241 AA: 27021 MW: 781D333692C3EE97 CRC64;

Query Match 41.28; Score 441; DB 6; Length 241;
 Best Local Similarity 47.28; Pred. No. 8.2e-32;
 Matches 102; Conservative 30; Mismatches 78; Indels 6; Gaps 4;

QY 1 MNSFSTSAF--GPAFSLGLLVLPAPFAPVPFGEDSKDVAAPHRQPLTSSERIDKQIR 58
 DB 1 MNSF-TSALRPGPLGSLALLVATFPTSAFVREDSKTSKSPK-TLTPGGTISIR 58
 QY 59 YLIDGISALAKRECNKSNKCESEKALAEENNLNPKMAEKDCGFCGSGNEETCLVKITITG 118
 DB 59 SILFTIKELREKMDHDHVNOMNKKALAEVNLILPLIEEDGCFPPAVANNETCLRLTSG 118
 QY 119 LLEFEVLEYLQNRFFESSEQARA--VQNSTKVLQIQLQKRNKLDATTPPTNASL 176
 DB 119 LMERMTLEHLOAKFRSDERNTSVSNLNIQHLILKTLRPKKNLNEATLKPAAVAVSM 178
 QY 177 TKLAQONQMDMTTHLILRSKFELQSSLRALRQ 212
 DB 179 ENLQKNQMLKTTIHLILGLTNFLETLRAVDLM 214

RESULT 10
 Q9WV08 PRELIMINARY; PRT: 210 AA.
 ID Q9WV08
 AC Q9WV08;


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DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Syviliagus auduboni1 (desert cottontail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Syviliagus.
OC NCBI_TaxID=30581;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT *The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169177; AAF86661.1; -.
DR InterPro: IPR003573; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA: 13763 MW: 9DDBC812ED31049 CRC64;

Query Match
Best Local Similarity 45.8%; Score 260; DB 6; Length 118;
Matches 54; Conservative 21; Mismatches 41; Indels 2; Gaps 1;

OY 97 EKDCFGSGFNEETCLVKITITGLLEFVYLEYLQNRPSSSEBOARA--VONSTVLIQFL 154
DB 1 EEDCFPLANHETCLRTISGLERFMYLEHLQAKFSEKENTRVSMILKNMHLINTL 60
OY 155 OKKAKNDATITPDPTTNSLTKLQANQMLQDMTHILRSFEFIQSSLRALROM 212
DB 61 RPKVKNNEGVTLPKPAVAVSLMNLQOKDMKMTTIFILRGLTDFLOFLRSVRILM 118

RESULT 14
O9MZ05 PRELIMINARY: PRT: 145 AA.
AC O9MZ05:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN, LYMPH NODES;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT *The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169184; AAF74824.1; -.
DR InterPro: IPR003573; -.
DR InterPro: IPR003574; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 145 AA: 16526 MW: 9679314A2AD3F01C CRC64;

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Query Match
Best Local Similarity 45.8%; Score 257; DB 6; Length 145;
Matches 54; Conservative 19; Mismatches 43; Indels 2; Gaps 1;

OY 97 EKDCFGSGFNEETCLVKITITGLLEFVYLEYLQNRPSSSEBOARA--VONSTVLIQFL 154
DB 1 EEDCFPLANHETCLRTISGLERFMYLEHLQAKFSEKENTRVSMILKNMHLINTL 60
OY 155 OKKAKNDATITPDPTTNSLTKLQANQMLQDMTHILRSFEFIQSSLRALROM 212
DB 61 RPKVKNNEGVTLPKPAVAVSLMNLQOKDMKMTTIFILRGLTDFLOFLRSVRILM 118

RESULT 15
O9MZ09 PRELIMINARY: PRT: 118 AA.
AC O9MZ09:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Syviliagus nuttallii (mountain cottontail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Syviliagus.
OC NCBI_TaxID=50378;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT *The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169178; AAF86662.1; -.
DR InterPro: IPR003573; -.
DR InterPro: IPR003574; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA: 13834 MW: 62E97FD3BDEABEC CRC64;

Query Match
Best Local Similarity 44.9%; Score 253; DB 6; Length 118;
Matches 53; Conservative 22; Mismatches 41; Indels 2; Gaps 1;

OY 97 EKDCFGSGFNEETCLVKITITGLLEFVYLEYLQNRPSSSEBOARA--VONSTVLIQFL 154
DB 1 EEDCFPLANHETCLRTISGLERFMYLEHLQAKFSEKENTRVSMILKNMHLINTL 60
OY 155 OKKAKNDATITPDPTTNSLTKLQANQMLQDMTHILRSFEFIQSSLRALROM 212
DB 61 RPKVKNNEGVTLPKPAVAVSLMNLQOKDMKMTTIFILRGLTDFLOFLRSVRILM 118

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Job time: 1186 sec

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PS Disclosure: Fig 1; 41pp: English.

CC The sequences in AAR3378-85 cytokines derived from the cytokine
CC family members leukemia inhibitory factor (LIF), granulocyte colony
CC stimulating factor (G-CSF), Interleukin-6 (IL-6) and oncostatin-M
CC (OSM). These cytokines were used in the production of hybrid
CC cytokines which have unique physiological properties. The hybrid
CC cytokines comprise a first, second, third and fourth alpha-helical
CC region derived from the corresponding region of one of the cytokines
CC given each derived from a factor different from that which at least
CC one additional region of the cytokine is derived.

XX Sequence 211 AA:

Query Match 100.0%; Score 1098; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.8e-100;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKPLSARDFHPVAFGLMLVTTAPPTSOVRGDFEDTTPRRPYTTSOYGGITHTVW 60
DB 1 mkflsardfhpvalglmlvttafpstgyrrgdfedtprrpyttsyvggiltvhw 60
OY 61 EIVEMKRELNGNSDCNNDDALAEENNLKLPETQRNDGCYGTGYNOEICLLKISSGLE 120
DB 61 eivemkrelcngnsdcnnddalaennlklpelqrndgcygtgyngelcilkissgley 120
OY 121 HSYLEYMKNMLKDKKKDKARVLRDTELIHFNOEKRLKIVLPPTISNALLTDKLES 180
DB 121 hsyleymknmlkdkkkdkarvlrdetclihfngevkdkhivlpptisnalltdkles 180
OY 181 QKEWLRTKTIOFILKSLPEFLKVTLASTROT 211
DB 181 qkewlrktlqfilkslpeflkvtlastrot 211

RESULT 2

AMR49040
ID AAR49040 standard; protein; 211 AA.

XX AAR49040:

DT 06-SEP-1994 (first entry)

XX Murine Interleukin-6.

DE Interleukin 6; IL-6; thrombocytopoiesis; surgery; chemotherapy;
KW radiation therapy; bone marrow transplantation; cancer therapy;
KW neoplasia; anti-neoplastic activity.

XX Mus musculus.

OS M09403492-A.

PN 17-FEB-1994.

PD 01-JUL-1993; 93MO-AU00324.

XX 06-AUG-1992; 92AU-0003983.

PR (LUDM-) LUDMIG INST CANCER RES.

PA (UYME) UNIV MELBOURNE.

XX Simpson RJ, Williams NT;

XX WPI: 1994-065607/08.

DR N-PSDB: AA055972.

XX New Interleukin-6 variants - capable of stimulating
PT thrombocytopoiesis while exhibiting low hydridoma growth factor
PT activity

XX Disclosure: Page 31; 46pp: English.

XX This sequence is murine Interleukin-6 (IL-6). IL-6 variants in
CC the form of non-full length molecules can stimulate, enhance or
CC facilitate thrombocytopoiesis without the side effects of other IL-6
CC activities. The IL-6 variants are useful for inducing
CC thrombocytopoiesis in thrombocytopenic patients following surgery,
CC chemotherapy, radiation therapy or bone marrow transplantation. The
CC IL-6 variants may also be useful in cancer therapy where the
CC fragments express anti-neoplastic activity.

XX Sequence 211 AA:

Query Match 100.0%; Score 1098; DB 15; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.8e-100;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKPLSARDFHPVAFGLMLVTTAPPTSOVRGDFEDTTPRRPYTTSOYGGITHTVW 60
DB 1 mkflsardfhpvalglmlvttafpstgyrrgdfedtprrpyttsyvggiltvhw 60
OY 61 EIVEMKRELNGNSDCNNDDALAEENNLKLPETQRNDGCYGTGYNOEICLLKISSGLE 120
DB 61 eivemkrelcngnsdcnnddalaennlklpelqrndgcygtgyngelcilkissgley 120
OY 121 HSYLEYMKNMLKDKKKDKARVLRDTELIHFNOEKRLKIVLPPTISNALLTDKLES 180
DB 121 hsyleymknmlkdkkkdkarvlrdetclihfngevkdkhivlpptisnalltdkles 180
OY 181 QKEWLRTKTIOFILKSLPEFLKVTLASTROT 211
DB 181 qkewlrktlqfilkslpeflkvtlastrot 211

RESULT 3

AMW95013
ID AMW95013 standard; peptide; 188 AA.

XX AMW95013:

DT 21-MAY-1999 (first entry)

XX Mouse Interleukin-6 (IL-6) polypeptide.

DE Cytokine; Interleukin-B30 (IL-B30); forensic science; cell proliferation;
KW inflammatory condition; drug screening; human; IL-6.

XX Mus sp.

OS W09905280-A1.

PN 04-FEB-1999.

PD 24-JUL-1998; 98MO-US15423.

XX 25-JUL-1997; 97US-0900905.

PR (SCHE) SCHERING CORP.

PA Bazan JF;

XX WPI: 1999-142935/12.

XX Newly isolated or recombinant polynucleotide encoding mammalian
PT cytokine Interleukin-B30 (IL-B30), including fragments - useful for
PT regulating activation, development, differentiation and function of
PT various cell types, and for diagnosing and treating conditions
PT associated with IL-B30

XX Disclosure: Page 11-12; 83pp: English.

XX This invention relates to mammalian cytokine Interleukin-B30 (IL-B30)
CC polypeptides. Host cells containing a vector comprising the IL-B30

CC nucleic acids are used for the recombinant production of the proteins.
 CC The polynucleotides are useful for diagnosis of IL-8/30 mediated
 CC conditions, and forensic science (e.g. to distinguish rodent from human,
 CC or as a marker to distinguish between different cells exhibiting
 CC differential expression or modification patterns). The IL-8/30 (including
 CC fragments), together with antibodies that bind to IL-8/30 are useful for
 CC teaching purposes. They are also used for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions. The polypeptide cytokine should mediate cytokine synthesis
 CC and proliferation in cells. IL-8/30 is useful for drug screening to
 CC identify compounds having binding affinity to IL-8/30. The present
 CC sequence represents a human IL-6.
 CC
 CC Sequence 188 AA:
 S0
 Query Match 89.4%; Score 982; DB 20; Length 188;
 Best Local Similarity 100.0%; Pred. No. 8,3e-89;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 24 APTSQVRGRGDEFTDPNRPVYTTSOVGLTHVLMELVEMKELCNGNSDCMNDAL 83
 |||
 Db 1 afptsqvrrgdfteftdpnrpyttsqvgllthvlwelmekelcngnsdcmndal 60
 OY 84 AENNNLKPEIORNDGCYOTGYNOEICLKISSGLIEVHSEVYMKNNLNDKRDARVIO 143
 |||
 Db 61 aennlkpeiorndgcycgtgyngetcllkissgllieyhnsleykmnkldkdkkarviq 120
 OY 144 RDETLIHIFNOEYKDLKIVLPPTISNALLTDLKESQKEMLRKTIOFLKSLSEFLKV 203
 |||
 Db 121 rdtetlihtfngexvdkhkiivlpptisnalltdkiesqkewlrktitqiflkisleeifkv 180
 OY 204 TLSTROT 211
 |||
 Db 181 tlrstrot 188
 RESULT 4
 AAR06847
 ID AAR06847 standard; protein: 211 AA.
 XX
 AC AAR06847;
 DT 14-JAN-1991 (first entry)
 DE XX
 DE Rat interleukin-6 (IL-6).
 DE XX
 KW Immunostimulant; antitumour; antiinflammatory; cytokine.
 KW XX
 OS Rattus rattus.
 OS XX
 PN JP02195885-A.
 PN XX
 PD 02-AUG-1990.
 PD XX
 PF 25-JAN-1989; 89JP-0016806.
 PF XX
 PR 25-JAN-1989; 89JP-0016806.
 PR XX
 PA (SAKA) OTSUKA PHARM KK.
 PA XX
 DR WPI; 1990-278846/37.
 DR XX
 DR N-PSDB; AAO05965.
 DR XX
 PT Rat IL-6 gene - used in development of IL-6 for drugs e.g.
 PT immunostimulant, antitumour drug, antiinflammatory drug etc.
 PT XX
 PS Claim 1; Page 553; 16pp; Japanese.
 PS XX
 CC IL-6 gene product may be useful in study and development of
 CC drugs eg. immunostimulants, antitumour drugs, cytokine production
 CC accelerators, antiinflammatory drugs and radiation damage inhibitors.
 CC XX

S0 Sequence 211 AA:
 Query Match 86.0%; Score 944; DB 11; Length 211;
 Best Local Similarity 85.3%; Pred. No. 5,3e-85;
 Matches 180; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
 OY 1 MKFLSRDRHPVAFGLMLVTTTAPPTSQVRGRGDEFTDPNRPVYTTSOVGLTHVLM 60
 |||
 Db 1 mkflsrdrhpvafglmlvtttappptsqvrrgdfteftdpnrpyttsqvgllthvlylr 60
 OY 61 EIVEMKRELCSGNSDCMNDALAEENNLKPEIORNDGCYOTGYNOEICLKISSGLIEY 120
 |||
 Db 61 eivemkrelcngnsdcmndalaeennlkpeiorndgcycgtgyngetcllkissgllief 120
 OY 121 HSYLEVEMKNNLNDKNDKARVIOBDETLIHIFNOEYKDLKIVLPPTISNALLTDLKES 180
 |||
 Db 121 rhyetvkmnqdkdkkarviqstetclvhtkqelsykvivlpptisnallmekies 180
 OY 181 OKEMLRKTIOFLKSLSEFLKVTLSTROT 211
 |||
 Db 181 qkewlrktitqiflkisleeifkvmlrstrot 211
 RESULT 5
 AAB49786
 ID AAB49786 standard; Protein: 212 AA.
 XX
 AC AAB49786;
 DT 23-APR-2001 (first entry)
 DE XX
 DE Human interferon beta 2a (IL-6) amino acid sequence.
 DE XX
 KW Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
 KW immune system related disorder; cancer; multiple sclerosis; AIDS;
 KW hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
 KW diabetes; allergy; chronic myelogenous leukaemia.
 KW XX
 OS Homo sapiens.
 OS XX
 PN WO200107608-A1.
 PN XX
 PD 01-FEB-2001.
 PD XX
 PF 20-JAN-2000; 2000WO-US01239.
 PF XX
 PR 21-JUL-1999; 99US-0358587.
 PR XX
 PR 21-JUL-1999; 99WO-US16424.
 PR XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA XX
 PI Ruben SM, Moore PA, Lafleur DW;
 PI XX
 DR WPI; 2001-138557/14.
 DR XX
 PT Isolated keratinocyte derived interferon protein and polynucleotide
 PT used to prevent, treat or ameliorate an immune system related disorder,
 PT viral infection, viral exposure and cancer -
 PT XX
 PS Disclosure; Fig 4; 303pp; English.
 PS XX
 CC This invention relates to human polynucleotide sequence AAF72333 which
 CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
 CC a member of the interferon family. AAF72338 represents the codon
 CC optimised sequence of KDI. The human KDI gene is located on chromosome 9.
 CC The specification includes KDI related protein sequences
 CC AAB49775 - AAB49789. Also given in the specification are primer, probe
 CC and polynucleotide sequences represented by AAF72334-AAF72370 (excluding
 CC AAF72338) which are used in the isolation and characterisation of the KDI
 CC sequence of the invention. The KDI polypeptide is used to treat viral
 CC infections and the protein and polynucleotide may be used to prevent,
 CC treat or ameliorate a medical condition such as immune system-related


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DE Interleukin-6.
XX Interleukin-6; lysine-depleted variant;
KW site-directed mutagenesis; human.
XX
XX Homo sapiens.
XX MO8905824-A.
XX
XX 29-JUN-1989.
XX
XX 22-DEC-1988; 88MO-US04633.
XX
XX 23-DEC-1987; 87US-0137043.
XX
XX (GENE ) GENETICS INST INC.
XX
XX Shaw G;
XX
XX WPI: 1989-206594/28.
XX
XX N-PSDB; AAN90235.
XX
XX New lysine depleted variants of polypeptide
XX - opt. modified with hydrophilic residues,
XX biologically active but with altered solubility, stability etc.
XX Disclosure; fig 3; 35pp; English.
XX
XX DNA of Interleukin-6 (see corresp. AAN90255). Used in the patent
XX to create lysine depleted variants by site-directed mutagenesis,
XX or synthesis.
XX
XX Sequence 212 AA;

Query Match 38.3%; Score 420.5; DB 10; Length 212;
Best Local Similarity 41.8%; Pred. No. 1.6e-33;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSARDHFHVAF-LGLMLVTTTAPPTSOVRRGDFTED-TTPNR-PVYTTSOVGLITH 57
DB 1 mnsfatsafgpvalfsllivlpadfp-apvppgedskvaaphrqpiltsearidkqiry 59
QY 58 VLMEIVEMRKELCGNSDCNMNDALAEENNLKLPETIORNDGCGYOTGYNOEICLKISSGL 117
DB 60 lldglsalrketckhsmcceskskcalaelnlnlpkmaekdgcfgsfneectlrvklltgi 119
QY 118 LEYHSYLEYMKNNLKDNKKDKARVLOQDTEYLHIHFNOEVKDLKIVLPPISNALLTDK 177
DB 120 lfevyleylygnrf-essseqaravymstkvllqfllqkxaknldaltlcpdptnasiltk 178
QY 178 LESQEWLRTKTIOFILKSLSEFLKVTLRSTRO 210
DB 179 lqaqngvlgdmthlllrstfkeflgsalralcq 211

RESULT 15
AAR05415
ID AAR05415 standard; protein; 212 AA.
XX
XX AAR05415;
XX
XX 27-JUL-1990 (first entry)
XX
XX Human B-cell differentiation factor gene product.
XX
XX BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
XX
XX Homo sapiens.
XX
XX JF02009388-A.
XX
XX 12-JAN-1990.
XX
XX

```

```

XX
XX 08-JUL-1988; 88JP-0170142.
XX
XX 09-MAR-1988; 88JP-0055270.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX WPI: 1990-055348/08.
XX
XX N-PSDB; AAO01763.
XX
XX Physiologically active protein prepn.
XX
XX PT by transforming plasmid having gene coding physiologically
XX PT active protein and gene of dihydrofolic acid reductase to hamster
XX PT ovary etc.
XX
XX Example 3; Fig 6; 12pp; Japanese.
XX
XX
XX Gene may be expressed by transforming a dhfr negative strain of CHO cells
XX CC with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product
XX CC is a B-cell differentiating factor.
XX
XX Sequence 212 AA;

Query Match 38.3%; Score 420.5; DB 11; Length 212;
Best Local Similarity 41.8%; Pred. No. 1.6e-33;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSARDHFHVAF-LGLMLVTTTAPPTSOVRRGDFTED-TTPNR-PVYTTSOVGLITH 57
DB 1 mnsfatsafgpvalfsllivlpadfp-apvppgedskvaaphrqpiltsearidkqiry 59
QY 58 VLMEIVEMRKELCGNSDCNMNDALAEENNLKLPETIORNDGCGYOTGYNOEICLKISSGL 117
DB 60 lldglsalrketckhsmcceskskcalaelnlnlpkmaekdgcfgsfneectlrvklltgi 119
QY 118 LEYHSYLEYMKNNLKDNKKDKARVLOQDTEYLHIHFNOEVKDLKIVLPPISNALLTDK 177
DB 120 lfevyleylygnrf-essseqaravymstkvllqfllqkxaknldaltlcpdptnasiltk 178
QY 178 LESQEWLRTKTIOFILKSLSEFLKVTLRSTRO 210
DB 179 lqaqngvlgdmthlllrstfkeflgsalralcq 211

Search completed: October 4, 2001, 18:52:09
Job time: 1675 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; Search time 32.27 Seconds

(without alignments) 134.632 Million cell updates/sec

Title: US-09-230-048-4

Perfect score: 1098

Sequence: 1 MKFLSARDHPVAFGLMLV.....FILKSLRFLKVTLRSTROT 211

Scoring table: BLOSUM62

Searched: 197339 segs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1098	100.0	211	4	US-08-097-869-8
2	982	89.4	188	3	US-09-122-443-14
3	420.5	38.3	212	1	US-08-792-0198-9
4	420.5	38.3	212	3	US-08-988-819-9
5	420.5	38.3	212	4	US-09-016-534-9
6	420.5	38.3	212	4	US-08-097-869-7
7	420.5	38.3	212	4	US-08-795-4738-6
8	420.5	38.3	212	4	US-08-795-4738-6
9	383	34.6	184	3	US-09-122-443-13
10	380	34.6	188	3	US-09-122-443-12
11	377.5	34.4	185	1	US-07-918-181A-4
12	377.5	34.4	185	5	PCT-US93-06928-4
13	377.5	34.4	185	5	PCT-US93-06928-4
14	375.5	34.2	185	1	US-07-918-181A-8
15	375.5	34.2	185	1	US-08-231-575-8
16	375.5	34.2	185	5	PCT-US93-06928-8
17	373.5	34.0	183	1	US-08-009-973-1
18	373.5	34.0	184	1	US-08-567-047-2
19	373.5	34.0	184	2	US-08-567-048-2
20	373.5	34.0	184	6	5186931-1
21	373.5	34.0	185	1	US-07-632-0708-1
22	373.5	34.0	185	1	US-07-918-181A-2
23	373.5	34.0	185	1	US-08-231-575-2
24	373.5	34.0	185	1	US-08-246-427A-5
25	373.5	34.0	185	2	US-08-716-317-7
26	373.5	34.0	185	2	US-08-766-620-5
27	373.5	34.0	185	5	PCT-US93-06928-2

28	373.5	34.0	185	6	5186931-2	Patent No. 5186931
29	373.5	34.0	186	1	US-07-632-0708-2	Sequence 2, Appl
30	373.5	34.0	186	1	US-07-745-382-20	Sequence 20, Appl
31	373.5	34.0	186	1	US-07-921-848-20	Sequence 20, Appl
32	373.5	34.0	186	1	US-08-165-301A-20	Sequence 20, Appl
33	373.5	34.0	186	3	US-08-469-318-163	Sequence 163, App
34	373.5	34.0	186	3	US-08-468-609A-163	Sequence 163, App
35	373.5	34.0	186	4	US-08-810-436A-20	Sequence 20, Appl
36	373.5	34.0	186	5	PCT-US93-01183-163	Sequence 163, App
37	373.5	34.0	187	1	US-07-632-0708-3	Sequence 3, Appl
38	373.5	34.0	187	3	US-08-469-318-145	Sequence 145, App
39	373.5	34.0	317	5	US-08-468-609A-145	Sequence 145, App
40	373.5	34.0	317	5	PCT-US93-01185-145	Sequence 145, App
41	371.5	33.8	184	2	US-08-693-182-2	Sequence 2, Appl
42	371.5	33.8	184	2	US-09-008-482-2	Sequence 2, Appl
43	371.5	33.8	185	1	US-07-918-181A-6	Sequence 6, Appl
44	371.5	33.8	185	1	US-08-231-575-6	Sequence 6, Appl
45	371.5	33.8	185	1	US-08-231-575-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-097-869-8
Sequence 8, Application US/08097869
Patent No. 6204364
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,869
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/753,178
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24455-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-097-869-8

Query Match 100.0% Score 1098; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.5e-103;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKFLSARDHPVAFGLMLVTTTAPPTSOVRRGDFETDTPNRPVYTTSGVGLITHTVL 60

DB 1 MKFLSARFHFVAFGLMLVTTTAFPTSGVRGDDFTEDTPRPNVYTTSGVGLITHVLW 60
QY 61 FIVEKRRKELCGNSDCNNNDALAEENNLKLPETIORNDGCGYGTGNOEICLKISSGLLEY 120
DB 61 FIVEKRRKELCGNSDCNNNDALAEENNLKLPETIORNDGCGYGTGNOEICLKISSGLLEY 120
QY 121 HSYLEYKNNKNDKKKDKARAVLORDETLHIFNDEVKDLHKIVLPPISNALLTDKLES 180
DB 121 HSYLEYKNNKNDKKKDKARAVLORDETLHIFNDEVKDLHKIVLPPISNALLTDKLES 180
QY 181 OKEMLRRTTIOFILKSLEEFKVTLRSTROT 211
DB 181 OKEMLRRTTIOFILKSLEEFKVTLRSTROT 211

RESULT 2
US-09-122-443-14
; Sequence 14, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazern, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-122-443-14

Query Match 89.4%; Score 982; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.2e-91;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 APTPSQVRGDDFTEDTPRPNVYTTSGVGLITHVLWELVEKRRKELCGNSDCNNNDAL 83
QY 1 APTPSQVRGDDFTEDTPRPNVYTTSGVGLITHVLWELVEKRRKELCGNSDCNNNDAL 60
DB 84 AENNLKLPETIORNDGCGYGTGNOEICLKISSGLLEYHSYLEYKNNKNDKKKARAVLQ 143
QY 61 AENNLKLPETIORNDGCGYGTGNOEICLKISSGLLEYHSYLEYKNNKNDKKKARAVLQ 120
DB 144 RDTETLHIFNDEVKDLHKIVLPPISNALLTDKLESOKEMLRRTTIOFILKSLEEFKLV 203

DB 121 RDTETLHIFNDEVKDLHKIVLPPISNALLTDKLESOKEMLRRTTIOFILKSLEEFKLV 180
QY 204 TLRSTROT 211
DB 181 TLRSTROT 188

RESULT 3
US-08-792-019B-9
; Sequence 9, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; NAME/KEY: Region
; LOCATION: -30..0
; US-08-792-019B-9

Query Match 38.3%; Score 420.5; DB 1; Length 212;
Best Local Similarity 41.8%; Pred. No. 9.4e-35;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSARDFHFVAF-LGLMLVTTTAFPTSGVRGDDFTED-TTPNR-PVYTTSGVGLITH 57
DB 1 MNSFSTSAFQVAFSLDILLVLPAPR-APVPGEDSKVAPRHPROTSSERIDKQIR 59
QY 58 VLMEIVEKRRKELCGNSDCNNNDALAEENNLKLPETIORNDGCGYGTGNOEICLKISSGL 117
DB 60 ILDDISALRKRTCKSKSMCSKALAEENNLKPKAEKNDGCGFGSGFNEFCVKKITGL 119
QY 118 HSYLEYKNNKNDKKKDKARAVLORDETLHIFNDEVKDLHKIVLPPISNALLTDK 177
DB 120 LEPEYLEYLYONR-ESSEDOARAVOMSTKVLIOFLQKKAKMLDAITTPDPTNASILTK 178
QY 178 LESOKEMLRRTTIOFILKSLEEFKVTLRSTROT 210
DB 179 LQADONMLQDMTHLILRSRFRFLOSSLRALQ 211

	Query Match	38.3%	Score 420.5	DB 6	length 212
	Best Local Similarity	41.8%	Pred. No. 9.4e-35		
	Matches	89	Conservative	50	Mismatches 69
					Indels 5
					Gaps 5
Oy	1	MKFLSARDPHVAF-VGLMLVTTTAPPSVORRGFTFD-TTPPR-PVYTTSGVGLITH	57		
		1			
Db	1	MNSRSTSAFSPVAFSLGLLVLPAAFP-APVPGRDSDVAAPRQGLVTSERIDQIR	59		
Oy	58	VIMVIVMRELCNGSDGNNDDLAENKIKIPICQNDGCVGTGNOEICLKISSGL	117		
		1			
Db	60	ILDGSLAKRETCNKSNKCESSKEALAKENLLPAPMAKDCGFGSGNETCLVKTIGL	119		
Oy	118	LEHASTLEYTKKNNLKNKKDKKARVILQRTETLITIFMDEVADLKIYVLPPISSALLTDK	177		
		1			
Db	120	DEFEVYLETQNNF-ESSEQAAYQVMSKTVILQFLQKANKNDALITTPPTNASLTK	178		
Oy	178	LESQKEMLRKTIQFLTKSLPEELKVTYLRSTQ	210		
		1			
Db	179	LQAGQNALQDMTHLLILRSFKFELSSALRQ	211		

RESULT 9
 US-09-122-443-13
 : Sequence 13, Application US/09122443
 Patent No. 6060284
 : GENERAL INFORMATION:
 APPLICANT: Bazan, J. Fernando
 TITLE OF INVENTION: MAMMALIAN CYTOKINE: RELATED REAGENTS
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/122,443
 FILING DATE: 24-JUL-1998
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/053,765
 FILING DATE: 25-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Chang, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX075BK1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-122-443-13

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Query Match      34.9%   Score 383; DB 3; Length 184;
Best Local Similarity 40.1%; Pseq No. 4,6e-31;
Matches 75; Conservative 44; Mismatches 62; Indels 6; Gaps 3

OY      24 AAPPQSQRGDFEDTTPNPNVYT--SQVGSLITVLWLYEMRKELCNGSDCMNDDA 82
          ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1 AAPPGPLGEGFNKDDTPSRLLTPEKTEALAIKIIVKISAIRKELECKNDENSKET 60

```

[illegible]

```

1  RESULT 10
2  US-09-122-443-12
3  : Sequence 12, Application US/09122443
4  : Patent No. 6060264
5  : GENERAL INFORMATION:
6  : APPLICANT: Bazan, J. Fernando
7  : TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
8  : NUMBER OF SEQUENCES: 16
9  : CORRESPONDENCE ADDRESS:
10 : ADDRESSEE: DNAX Research Institute
11 : STREET: 901 California Avenue
12 : CITY: Palo Alto
13 : STATE: California
14 : COUNTRY: USA
15 : ZIP: 94304-1104
16 : COMPUTER READABLE FORM:
17 : MEDIUM TYPE: Floppy disk
18 : COMPUTER: IBM PC compatible
19 : OPERATING SYSTEM: PC-DOS/MS-DOS
20 : SOFTWARE: PatentIn Release #1.0, Version #1.30
21 : CURRENT APPLICATION DATA:
22 : APPLICATION NUMBER: US/09/122.443
23 : FILING DATE: 24-JUL-1998
24 : CLASSIFICATION: 436
25 : PRIOR APPLICATION DATA:
26 : APPLICATION NUMBER: US 60/053,765
27 : FILING DATE: 25-JUL-1997
28 : ATTORNEY/AGENT INFORMATION:
29 : NAME: Ching, Edwin P.
30 : REGISTRATION NUMBER: 34,090
31 : REFERENCE/DOCKET NUMBER: DX0756K1
32 : TELECOMMUNICATION INFORMATION:
33 : TELEPHONE: (650)852-9196
34 : TELEFAX: (650)496-1200
35 : INFORMATION FOR SEQ ID NO: 12:
36 : SEQUENCE CHARACTERISTICS:
37 : LENGTH: 188 amino acids
38 : TYPE: amino acid
39 : STRANDEDNESS: single
40 : TOPOLOGY: linear
41 : MOLECULE TYPE: peptide
42 : US-09-122-443-12

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[illegible]

Fri Oct 5 10:02:15 2001

us-09-230-048-4.rai

Page 8

OY 151 HENOEVKDLIKIVLPTISNALLTDXLESOKEMWLRKTIQFIILKSLEEFKVITRSTRO 210
:: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 125 QPLQKKAKNLDATPPDPPTNNASLTLTKIQAOQNWLQDMWTHLLIRSLKEPMSSIALRQ 184

Search completed: October 4, 2001, 19:10:32
Job time: 1163 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:55 Search time 44.98 seconds
(without alignments)
357.333 Million cell updates/sec

Title: US-09-230-048-4
Perfect score: 1098
Sequence: 1 MKFLSARDFHPVAFGLMLV.....FLKSLLEFLKVLTRSTROT 211

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1098	100.0	211	1	ICMS6
2	944	86.0	211	2	A34247
3	432.5	39.4	212	2	I46590
4	428.5	39.0	212	2	I46621
5	422.5	38.5	208	1	A56610
6	420.5	38.3	208	1	S29549
7	420.5	38.3	212	1	I46621
8	414.5	37.8	208	2	T09216
9	337	30.7	207	2	I46084
10	96	8.7	819	2	T19351
11	95	8.7	201	2	A42247
12	93.5	8.5	534	2	S57974
13	92.5	8.4	261	2	B64746
14	91.5	8.3	2663	1	S28261
15	90.5	8.2	1127	2	T28317
16	90.5	8.2	2042	2	T18399
17	86.5	7.9	480	2	H86411
18	86.5	7.9	743	2	D84545
19	85.5	7.8	1516	2	E71619
20	85	7.7	2401	2	T28676
21	84.5	7.7	1156	2	B70356
22	84.5	7.7	1228	2	A57384
23	84	7.7	636	2	H70184
24	84	7.7	783	2	T23452
25	84	7.7	785	2	T23456
26	84	7.7	1186	2	T27075
27	84	7.7	1354	2	S74244
28	83.5	7.6	162	2	H71486
29	83.5	7.6	1354	2	S69211

30	83.5	7.6	1417	2	T18418	hypothetical prote
31	83.5	7.6	1532	2	T18438	hypothetical prote
32	83	7.6	1170	2	A56157	chromosome segrega
33	83	7.6	2304	2	T07920	probable acetyl-Co
34	83	7.6	8243	2	T31307	type I fatty acid
35	82.5	7.5	750	2	T38435	collared coil protei
36	82.5	7.5	911	2	JC7186	alpha-actinin-4 -
37	82.5	7.5	1076	2	C70007	hypothetical prote
38	82	7.5	720	2	JC6562	heat shock protein
39	82	7.5	758	2	S60586	glucocorticoid rec
40	82	7.5	1365	2	T18419	hypothetical prote
41	81.5	7.4	326	2	S49377	hypothetical prote
42	81.5	7.4	594	2	A82913	hypothetical prote
43	81.5	7.4	635	2	G86589	hypothetical prote
44	81.5	7.4	635	2	G72035	regulatory protein
45	81	7.4	176	2	A56652	interleukin-7 prec

ALIGNMENTS

RESULT 1

ICMS6
Interleukin-6 precursor - mouse
N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepat acyloma growth factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 22-Jun-1999
C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799;
R:Tanabe, O.; Akira, S.; Kamitaya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of poten
A:Reference number: A30531; MUID:89055525
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <TAN>
A:Cross-References: GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.;
Eur. J. Immunol. 18, 193-197, 1988
A:Title: CDNA cloning of murine interleukin-Hp1: homology with human interleukin 6.
A:Reference number: A27610; MUID:88166883
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-References: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.;
J. Immunol. 142, 1372-1376, 1989
A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOCK>
A:Cross-References: GB:M24221; NID:g341131; PIDN:AA66814.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rudira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence an
A:Reference number: S01323; MUID:8832059
A:Accession: S01323
A:Molecule type: protein
A:Residues: 25-165 'X' 168-211 <SIM>
A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 10
Nucleic Acids Res. 18, 6455, 1990
A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MUID:91057159
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <GRS>
A:Cross-References: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleav
A:Reference number: A30157; MUID:90147691

A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75:78-94:128-148 <JA5>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Juttenhove, C.; Coulie, P.G.; Rubira, M.R.; Stimp
 Proc. Natl. Acad. Sci. U.S.A. 83: 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Reference number: A26652; MUID:87092311
 A:Accession: A26652
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85: 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A40486; MUID:89017145
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CH12>
 A:Cross-references: GB:J03783; NID:9198367; PIDN:AA39301.1; PID:9309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72: 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein Mcl-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171: 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mc
 A:Reference number: S10241; MUID:90171860
 A:Accession: S10241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:949738; PIDN:CA55824.1; PID:9581860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217: 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin
 A:Reference number: S38254; MUID:94039075
 A:Accession: S38254
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60/75, 'X', 77-79, 176-203 <2HA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Introns: 7/1: 68/3; 156/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine;
 F:1-24/Domain: signal sequence #status predicted <Sig>
 F:23-211/Product: Interleukin-6 #status experimental <Mat>

Query Match 100.0%; Score 1098; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5, 2e-82;
 Matches 211: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFLSADFPVAFGLMLVTTTAPTSQVRGDFTEPTNRPVYTTTSGVGLITHTVM 60
 DB 1 MKFLSADFPVAFGLMLVTTTAPTSQVRGDFTEPTNRPVYTTTSGVGLITHTVM 60
 QY 61 EIVEMRKELCNGSDCNDNDALAEENNLKLPETQNRDCCYGTGNOEICLKISSGLLEY 120
 DB 61 EIVEMRKELCNGSDCNDNDALAEENNLKLPETQNRDCCYGTGNOEICLKISSGLLEY 120
 QY 121 HSYLEYKNNLKNNKDKARVLRQDTEFLIHFNQEVADLKIVLPPISNALLTDLKES 180
 DB 121 HSYLEYKNNLKNNKDKARVLRQDTEFLIHFNQEVADLKIVLPPISNALLTDLKES 180
 QY 181 QKEWLRKTKTQFLKSLSEFLKVTLRSTROT 211
 DB 181 QKEWLRKTKTQFLKSLSEFLKVTLRSTROT 211

RESULT 2
 A34247
 Interleukin-6 precursor - rat
 N:Alternate names: IL-6
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
 A:Accession: A34247
 R:Northemann, W.; Bracklak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
 J. Biol. Chem. 264: 16072-16082, 1989
 A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-der
 A:Reference number: A34247; MUID:89380206
 A:Accession: A34247
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-211 <NOR>
 A:Cross-references: GB:M2744; NID:9204915; PIDN:AA77659.1; PID:9204916
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 86.0%; Score 944; DB 2; Length 211;
 Best Local Similarity 85.3%; Pred. No. 1, 6e-69;
 Matches 180: Conservative 18; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MKFLSADFPVAFGLMLVTTTAPTSQVRGDFTEPTNRPVYTTTSGVGLITHTVM 60
 DB 1 MKFLSADFPVAFGLMLVTTTAPTSQVRGDFTEPTNRPVYTTTSGVGLITHTVM 60
 QY 61 EIVEMRKELCNGSDCNDNDALAEENNLKLPETQNRDCCYGTGNOEICLKISSGLLEY 120
 DB 61 EIVEMRKELCNGSDCNDNDALAEENNLKLPETQNRDCCYGTGNOEICLKISSGLLEY 120
 QY 121 HSYLEYKNNLKNNKDKARVLRQDTEFLIHFNQEVADLKIVLPPISNALLTDLKES 180
 DB 121 HSYLEYKNNLKNNKDKARVLRQDTEFLIHFNQEVADLKIVLPPISNALLTDLKES 180
 QY 181 QKEWLRKTKTQFLKSLSEFLKVTLRSTROT 211
 DB 181 QKEWLRKTKTQFLKSLSEFLKVTLRSTROT 211

RESULT 3
 I46590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 A:Accession: I46590
 R:Mathalagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32: 324-330, 1992
 A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co
 A:Reference number: I46590; MUID:92360284
 A:Accession: I46590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAT>
 A:Cross-references: GB:M80258; NID:9164514; PIDN:AAC27127.1; PID:9164515
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6
 Query Match 39.4%; Score 432.5; DB 2; Length 212;
 Best Local Similarity 42.7%; Pred. No. 4, 9e-28;
 Matches 90: Conservative 42; Mismatches 76; Indels 3; Gaps 3;
 QY 1 MKFLSADFPVAFGLMLVTTTAPTSQVRGDFTEPTNRPVYTTTSGVGLITHTVM 58
 DB 1 MNSLVSASFVAFGLILVMTATFPPPERLEDAKGDATSDKMLFTSPDKTEELIKYI 60
 QY 59 LMEIVEMRKELCNGSDCNDNDALAEENNLKLPETQNRDCCYGTGNOEICLKISSGL 118
 DB 61 LKISARKEKCEYKENCSEKVELAENNLMLPKVAEKDGCFOGFGNOEICLKIRTTGLV 120

DESC BOCAI IMMEDIATELY
7-2-70,
FEDU.
NO. 7-15

A;Residues: 1-212 <YAS>
A;Cross-references: GB:Y00081;

Cross-references: GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495

A:Note: the authors translated the codon CAG for residue 130 as Glu
 R.Zilberstein, A.; Ruggieri, R.; Kohn, J.H.; Revel, M.
 EMBO J. 5, 2529-2537, 1986
 A:Title: Structure and expression of cDNA and genes for human Interferon-beta-2, a distal
 A:Reference number: A91051; MUID:87053818
 A:Accession: A25692
 A:Molecule type: mRNA
 A:Residues: 1-212 <21L>
 A:Cross-references: GB:X04430; NID:932673; PIDN:CAA28026.1; PID:932674
 R.Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Melanabe, Y.; Matsuda, T.; Kishimoto, T.
 Nature 324, 73-76, 1986
 A:Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymphocy
 A:Reference number: A93387; MUID:87065033
 A:Accession: A26966
 A:Molecule type: protein
 A:Residues: 1-212 <H1R>
 A:Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
 R.Tomonouchi, N.; Mlwa, K.; Katsuyama, H.; Matsui, H.
 Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
 A:Title: Detection of 3' untranslated region of human BSF-2 mRNA causes stabilization of
 A:Reference number: A33515; MUID:89391958
 A:Accession: A33515
 A:Molecule type: mRNA
 A:Residues: 1-212 <TON>
 A:Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
 R.Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
 Eur. J. Biochem. 159, 625-632, 1986
 A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h
 A:Reference number: A25801; MUID:87004683
 A:Accession: A25801
 A:Molecule type: DNA; mRNA
 A:Residues: 1-212 <HAEG>
 A:Cross-references: GB:X04403
 A:Experimental source: fibroblast
 R.May, L.T.; Helfgott, D.C.; Sehgal, P.B.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A:Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:9184628; PIDN:AAA52728.1; PID:9306910
 R.Mong, G.G.; Mitek-Glanoff, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Biochim. Biophys. Res. Commun. 139, 4116-4121, 1987
 A:Title: Interleukin 6: identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317
 A:Accession: I52193
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:9186351; PIDN:AA41704.1; PID:9186352
 R.Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A:Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
 A:Reference number: I56003; MUID:88088768
 A:Accession: I56003
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: protein
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:9184631; PIDN:AAA52729.1; PID:9306911
 R.Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snelck, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A:Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', '53-57', 'X', '59', 'X', '61 <VAN1>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', '59-61', 'X', '63 <VA2>
 R.Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990

A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involv
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <RAM>
 R.Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody a
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R.Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takeuchi, K.; Hara, T.; Ishikawa, H.;
 Anticancer Res. 11, 961-968, 1991
 A:Title: Purification and characterization of human fibroblast derived differentiatio
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NDP>
 A:Experimental source: fibroblast
 R.Ming, J.E.; Gernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A:Title: Interleukin 6 is the principal cytokinetic T lymphocyte differentiation factor
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R.May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A:Title: Marked cell-type-specific differences in glycosylation of human Interleukin-
 A:Reference number: A48419; MUID:91355644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', '39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone
 A:Note: this 28-30k form contained both N-linked and O-linked carbohydrate; a 25k for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A:Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R.Brita, T.; Oheka, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A:Title: Polypeptide and carbohydrate structure of recombinant human Interleukin-6 pr
 A:Reference number: JX0305; MUID:9426765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R.Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A:Title: Disulfide structures of human Interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R.Rock, F.L.; Li, X.; Chong, B.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A:Title: Roles of disulfide bonds in recombinant human Interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; disulfide and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: It therefore appears to function as an autoregulator of cell grow
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:116
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth
 F:1-27/Domain: signal sequence; status predicted <SIG>
 F:28-212/Product: Interleukin-6, long form; status experimental <MAT1>
 F:30-212/Product: Interleukin-6, short form; status experimental <MAT5>
 F:72-78,101-111/Disulfide bonds: #status experimental

F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.3%; Score 420.5; DB 1; Length 212;
Best Local Similarity 41.8%; Pred. No. 4.6e-27;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

1 MKEFASARDEHVAE-IGLMLVTTAAPTQVRRGDFPED-TTPNR-PVYTSSQVGLLTH 57
1 MNSFTSAFGVAASLGLLVPAAP-APVPPGDSKDVAAHPROPFTSSERIKQIRY 59
58 VLMEIVEMRKELCNGNSDCMNDALAEENNLKLPETIORNDGCGYGTGNOELCKLSSGL 117
60 IIDGISAIRKEFCNSKNKCESSKEALAEENNLKPKMAEKDCGCGFNEETCLVLTIGL 119
118 LEHSHYLEYKNNLKDNRKARVLODTELLIHFNQEVKDLHKIVLPTPISNALLTDK 177
120 LEFEYLYLELDNR-ESSEDAKAVQMSKTVLQFLOKKAKNDAITTPDPTTNASLTK 178
178 LESQKEMLRRTIOFILKSLSEFLKVTLRSTRQ 210
179 LQAOQMWLODMTHLILRSFEKFLQSSLRALRQ 211

RESULT 8

Interleukin-6 precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C:Accession: T09216
R:Swiderski, C.E.; Horohov, D.W.
submitted to the EMBL Data Library, July 1996
A:Accession: T09216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <SWI>
A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388
C:Genetics:
A:Gene: IL-6
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor

Query Match 37.8%; Score 414.5; DB 2; Length 208;
Best Local Similarity 43.3%; Pred. No. 1.4e-26;
Matches 87; Conservative 46; Mismatches 61; Indels 7; Gaps 6;

11 PVAF-IGLMLVTTAAPTQVRRGDFPEDTTPNRPVYTTSS-QVGLITVLMELVEMRKE 68
11 PVAFSGLLVMAFP-PLPLGE--DETTSSGRLTTPADKORHKIKYILGKISALKNE 67
69 LQNSDCMNDALAEENNLKLPETIORNDGCGYGTGNOELCKLSSGLEHSHYLEYK 128
68 MKNNSKCSKEVLAENNLKPKMAEKDCGCGFNEETCLVLTIGLSEFOYLYLEIYQ 127
129 NNLLKNNKRAKAVLQRODTELLIHFNQEVKDLHKIVLPTPISNALLTDKLESGKEMLRK 188
128 NEFK-GEKENITMOISIKVLYOILMOKMKK-PEVTPPTPAKSSLLALHLSQNEMLKMT 185
189 TIOFILKSLSEFLKVTLRSTR 209
186 TWHILRLSELDLPFSLRAVR 206

RESULT 9

Interleukin 6 - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I46084

R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204: 301-305, 1993
A:Title: Molecular cloning and characterization of a cDNA encoding feline interleukin 6
A:Accession: I46084
A:Reference number: I46084; MUID:94052249

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <BRA>
A:Cross-references: GB:I46914; NID:g438519; PIDN:AAI16620.1; PID:g438520
C:Superfamily: Interleukin-6

Query Match 30.7%; Score 337; DB 2; Length 207;
Best Local Similarity 35.4%; Pred. No. 2.7e-20;
Matches 75; Conservative 49; Mismatches 78; Indels 10; Gaps 6;

1 MKEFASARDEHVAE-IGLMLVTTAAPTQVRRGDFPEDTTPNR-PVYTSSQVGLITPV 58
1 MNLFTSAFSPALFSLGLLVATAFP-GLPGDITSRLPLTPADKMEELIKYI 56
59 LMEIVEMRKELCNGNSDCMNDALAEENNLKLPETIORNDGCGYGTGNOELCKLSSGL 118
60 LKISALKEKCMCDNKKCESSKEALAEENNLKPKMAEKDCGCGFNEETCLVLTIGL 116
118 LEHSHYLEYKNNLKDNRKARVLODTELLIHFNQEVKDLHKIVLPTPISNALLTDK 178
117 EFOYIYLFQIDKY-RGDKENAKSVYTSNVILQMLRKKNODEVITIPVYEVGL--OL 173
179 E-SQKEMLRRTIOFILKSLSEFLKVTLRSTR 209
174 SCSHRRVAEAVNNHLLRLRDLFOLRLRAVR 205

RESULT 10

Hypothetical protein C17E4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19351
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19113
A:Accession: T19351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-819 <ML>
A:Cross-references: EMBL:Z81037; PIDN:CAB02745.1; GSPDB:GN00019; CESP:C17E4.2
A:Experimental source: clone C17E4
C:Genetics:
A:Gene: CESP:C17E4.2
A:Map position: 1
A:Introns: 151/3; 346/3; 376/2; 446/3; 669/3; 707/3

Query Match 8.7%; Score 96; DB 2; Length 819;
Best Local Similarity 22.4%; Pred. No. 5;
Matches 46; Conservative 41; Mismatches 58; Indels 60; Gaps 11;

55 ITHVLMELVEMRKELCNGNSDCMNDALAEENNLKLPETIORNDGCGYGTGNOELCKLSSGLEHSHYLEYK 97
96 ITRVIEENALRKE--NNLKDITNNENIAKIGKNDKLDQEVKTDICKNKIKLEKDSMN 153
98 --GCGYGTGNO-ETCLKISSGLEHSHYLEYKNNNLK 132
154 PKISYVENSNTLELTOLKAENEFLK-HELVEQNPESMICKKEKFDLFTLEIMLNQVE 212
133 DNKKDKARVL---ORDT--ETLHFNQEVKDLHKIVLPTPISNALLTDKLESGKEMLR 186
213 ESFKKKMILAFDEKDSKEQMYLAKFREIDELKEIIDS-----VSUKLYNE--- 263
187 TKTIOFILKSLSEFLKVTLRSTRQ 211
264 TKACHSEIERLEDELKNNRDLRRS 288

RESULT 11

myelomonocytic growth factor precursor - chicken
 A:Accession: A42247
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-201 <STE>
 A:Note: sequence extracted from NCBI backbone (NCBI:89832, NCBI:89836)
 R:Leutz, A.; Damu, K.; Sternack, E.; Kowenz, E.; Nass, S.; Frank, R.; Gausepohl, H.; Par
 EMBO J. 8, 175-181, 1989
 A:Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals re
 A:Reference number: S03633; MUID:89231616
 A:Accession: A42247; MUID:92195319

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-201 <STE>
 A:Note: sequence extracted from NCBI backbone (NCBI:89832, NCBI:89836)
 R:Leutz, A.; Damu, K.; Sternack, E.; Kowenz, E.; Nass, S.; Frank, R.; Gausepohl, H.; Par
 EMBO J. 8, 175-181, 1989
 A:Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals re
 A:Reference number: S03633; MUID:89231616
 A:Accession: A42247; MUID:92195319

Query Match

Best Local Similarity 21.7%; Score 95; DB 2; Length 201;
 Matches 34; Conservative 29; Mismatches 74; Indels 20; Gaps 5;

QY 61 EIVKREKELGNSDGNNDALAEENNLKLPETGRNDCCYQYGNQFICLAKISSGLLEY 120
 DB 52 DVNADQRAVCDTFOLEECLOVOPDPLVQAPL-DQCHKGFQAEVCFQIRAGLHAY 110
 QY 121 HSYLEYKNNLKKKKDKARVLRQDTEFLIHIFNOEVD--LHKLVLP-----PISMA 172
 DB 111 HDSICAVL-RILPHTTTLVETLQIDANLSNLOOCEMEDLCIDVTLPAREGRSPPTFSG 169
 QY 173 LITDKLESQKEMLRKTIOFILKSLSEFLKVLLESTR 209
 DB 170 PFOOVGCG-----FFILANFQRFLETAVRALR 196

RESULT 12

hypochemical protein YDR147w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypochemical protein YB358.04
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
 C:Accession: S57974
 R:Murphy, L.; Richards, C.; Harris, D.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: S57971
 A:Accession: S57974
 A:Molecule type: DNA
 A:Residues: 1-534 <MUR>
 A:Cross-references: EMBL:Z50046; NID:g899393; PID:g899397; GSPDB:GN00004; MIPS:YDR147w
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: MIPS:YDR147w
 A:Map position: 4R

Query Match 8.5%; Score 93.5; DB 2; Length 534;
 Best Local Similarity 21.5%; Pred. No. 4.7;
 Matches 52; Conservative 47; Mismatches 68; Indels 75; Gaps 13;

QY 5 SARDHPVAFGLMLVTTTAPPTSOVNRGDF-----TEDTPNRPVYTT 48
 DB 81 TANDELKATVYNAKL--DPSLP-SQYFKODITINVLQSLIEPMSVPSGSKLNKLTL 137
 QY 49 SOVGGLTTHVLMEL-----VEKREKLGNSDGNNDALAEENNLKLPETGRNDCCYQ 101
 DB 138 TQIKGALTNIYKHPNLPPLLMR---IFGDS-----IDSVIRHEYLKVIARL-SFYD 188
 QY 102 TGYNOECLLKISSGLLEYHSLEYKNNLKKKKDKARVLRQDTEFLIHIFNOEVDLH 161
 DB 189 LGPRLP-----GFENKRFKYLEGSRSTQD---FIDROTSTIKI---AKKLEH 234
 QY 162 KIVLPPTISNALLTDK-----LESQKEM-----LRTKTIQFILKSL 198
 DB 235 CTV---PLTHKEITDQPCWTFPDQMKLIDSHKEMVNNVISENLGCSMNFELKSF 291
 QY 199 EF 200
 DB 292 NY 293

RESULT 13

yafr protein - Escherichia coli

C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
 C:Accession: B64746
 R:Blutner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: B64746
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-261 <BLAT>
 A:Cross-references: GB:AE000130; GB:U00096; NID:g1786402; PID:AA03321.1; PID:g17864
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: yafr
 C:Superfamily: Escherichia coli yafr protein

Query Match

Best Local Similarity 26.3%; Score 92.5; DB 2; Length 261;
 Matches 50; Conservative 26; Mismatches 81; Indels 33; Gaps 10;

QY 26 PTSQVRGDFTEETPN--RPVYTSQVGLITHVLMELVEKREL-CNGNSDGNND 81
 DB 82 PVILVOSGNRAPERIMQEMKRYTVSTFSG-----IDPRQPLTCNNKDKRNEED 133
 QY 82 ALAENNLKLPETGRNDCCYQYGNQFICLAKISSGLLEYHSLEYKNNL-KDKKXK-- 138
 DB 134 VASAEENNMQALRPVAA--KHOKAII---VYQMDLQGTDSALSTWSDTKNDKLT 188
 QY 139 ---ARVLRQDTEFLIHIFNOE-----VKDLHKIVLPPTISN-ALLTDKLESQKELRT 187
 DB 189 DAISLRYLVR--FLVDVATGEWATWSPVNYEKVLPPLDKNEASTDMTEQIMOLKQ 246
 QY 188 KTIOFILKSL 197
 DB 247 KTYKAWKDL 256

RESULT 14

centromere protein E - human

N:Alternate names: centromere 312K protein; kinesin-related protein CENP-E
 C:Species: Homo sapiens (man)
 C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
 C:Accession: S28261
 R:Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, L.; Cleveland, D.W.

Nature 359, 536-539, 1992

A:Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.

A:Reference number: S28261; MUID:93024922

A:Accession: S28261

A:Molecule type: mRNA

A:Residues: 1-2663 <P>N>

A:Cross-references: EMBL:Z15005; NID:g29864; PIDN:CAA78727.1; PID:g29865

C:Genetics:

A:Gene: GDB:CENPE

A:Cross-references: GDB:361164; OMIM:117143

A:Map position: 4q24-q25

C:Superfamily: centromere protein E; kinesin motor domain homology

C:Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop

F:7-35/Domain: kinesin motor domain homology <KMO>

F:86-93/Region: nucleotide-binding motif A (P-loop)

F:486-2183/Domain: coiled coil #status predicted <COI>

F:92/Binding site: ATP (Lys) #status predicted

Query Match 8.38; Score 91.5; DB 1; Length 2663;

Best Local Similarity 23.78; Pred. No. 48;

Matches 52; Conservative 39; Mismatches 73; Indels 55; Gaps 10;

OY 18 MLVTTTAPPTSQ-----VRGPTEDPTPNRPVTTTQVGGITPHV 58

DB 400 MLVTSSSLTLOELKAKKRRVWGLCKIKKMSNVADOF--NIPNTITTKHKISTNL 457

OY 59 LMEIYEMKELCNGSDCMNDALAEENLKLPEIORNDGCTGTGNOEICLKISSGLL 118

DB 458 LMEIDE--SVCSSEDFVPSNTLDLS-----EIEWNPATKL--LNOENIESLESLRA 505

OY 119 EYHASYL-----EYKNNLKD--NKKDKARVLQDPT-----TLIHIFNOEAKDLHK 162

DB 506 DYDNLVLYEQLRTEKEMELKKEKNDDEFELEKTKKQDEMQLIH-----EISNLKN 561

OY 163 IYLPPTISNALITDKLSQKEMLRTKTIQFIKLSLEEF 201

DB 562 LVKHHREYVNOLEMLSSKVELLREKEDQ--IKKIQEYI 598

RESULT 15

T28317

ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus

C:Species: Melanoplus sanguinipes entomopoxvirus

C:Date: 21-Jan-2000 #sequence, revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T28317

R:Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kulish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: 220484; MUID:99102612

A:Accession: T28317

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1127 <AFO>

A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97677.1; PID:g4049717

C:Genetics:

A:Note: MSV156

Query Match 8.28; Score 90.5; DB 2; Length 1127;

Best Local Similarity 26.08; Pred. No. 20;

Matches 40; Conservative 26; Mismatches 41; Indels 47; Gaps 9;

OY 61 EIVEKKEKELCNGSDCMNDALAEENLKLPEIORNDGCTGTGNOEICLKISSGLLEY 120

DB 444 DIIEELKN-----NNLOKLEENKKIDE-----QTEYKN---KINK---EX 478

OY 121 HSYLEYMKNNL---KDK--KDKARVLQDPTETLIHIFNO-----EYKDLKTIPLPTIS 170

DB 479 NDIEELKNNLOKLEENKNNIDKLTIKNDIESNTELFNKLNISDFKDSREIA----- 533

OY 171 NALITDKLSEKEMLRTKTIQFIKLSLEEF 204

DB 534 -----KLNTEVEQLRKDLLENINKT--NELMKLS 560

Search completed: October 4, 2001, 19:09:56
Job time: 1257 sec

Query Match	18.7%;	Score 205.5;	DB 6;	Length 118;
Best Local Similarity	36.0%;	Pred. No. 1.2e-10;		
Matches 41;	Conservative 29;	Mismatches 43;	Indels 1;	Gaps 1

RESULT	14	
Q9M2Q8		
ID	Q9M2Q8	PRELIMINARY;
		PRT; 118 AA

01-OCT-2000 (TEmblre). 15, Created)
 01-OCT-2000 (TEmblre). 15, last sequence update)
 01-MAR-2001 (TEmblre). 16, last annotation update)
 INTERLEUKIN 6 (FRAGMENT).
 IL-6
 Lepus californicus (Black-tailed jackrabbit).
 Eulazyrta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 NCBI_TaxID=48087;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=OVARY;
 MEDLINE=30304414; PubMed=10843729;
 Perkins H.D., van Leeuwen B.H., Hardy C.M., Kent P.J. :
 "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 European rabbit (Oryctolagus cuniculus).";
 Cytokine 12:555-565(2000).
 EMBL; AF169179; AAF86563.1; -.
 InterPro; IPR003574; -.
 Pfam; PF00489; IL6; 1.
 PRINTS; PR00433; IL6GSPWGF.
 PRINTS; PR00434; INTERLEUKIN6.
 PROSITE; PS00254; INTERLEUKIN_6; 1.
 SMART; SM00126; IL6; 1.
 NON_TER
 1
 SEQUENCE 118 AA: 13712 MW: 3EFFF2A9BD70A219 CRC64;

Query Match	18.2%;	Score 199.5;	DB 6;	Length 118;
Best Local Similarity	35.7%;	Pred. No. 4e-10;		
Matches	40;	Conservative	29;	Mismatches 42;
				Indels 1;
				Gaps 1

RESULT 15
Q9M2Q7
ID Q9M2Q7 PRELIMINARY; PRT: 118 AA

DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).

0S Lepus townsendii (White-tailed Jackrabbit).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
0X NCBI_TaxID=63225;

RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RX MEDLINE-20304414; PubMed-10843729;
RA PERKINS H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the

RL Cytokine 12:55-565(2000);
 DR EMBL: AF165180; AA066664.1; -.
 DR InterPro: IPR003573; -.
 DR InterPro: IPR003574; -.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PRO0433; IL6GCEPMGF.
 DR PRINTS: PRO0434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 FT NON-TER 1
 50 SSODNCE 118 AA: 1371 MW: 36FF2AF8D70A219 CRC64;

Query Match	18.2%	Score 199.5	DB 6	Length 118
Best Local Similarity	35.7%	Pred. No. 4e-10		
Matches 40; Conservative	29;	Mismatches 42;	Indels 1;	Caps 1

[illegible]

Search completed: October 4, 2001, 19:12:01
Job time: 1187 sec

OS Aotus nigricipes (black-headed night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
 RA Patarroyo M.E.;
 RT "Aotus nigricipes gene for IL-6."
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF097322; AAF21297.1; -
 DR HSSP: P05231; IAU.
 DR InterPro: IPR002069; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PRODOM: PD002435; -; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 175 AA: 19205 MW: 28CCE574CB99B189 CRC64;

Query Match 30.6%; Score 336.5; DB 6; Length 175;
 Best Local Similarity 42.4%; Pred. No. 8.3e-22;
 Matches 72; Conservative 33; Mismatches 62; Indels 3; Gaps 3;
 OY 1 MKFLSARDFHPVAF-LGLMLVTTTAPPTSGVRKDFTEDTTPRRPYT-TSGVGLITHV 58
 DB 1 MNSFSTSAFRPAFSLGILLVPAFPVPLGDSKEVAAPRQLTSTEDIDKHIRYI 60
 OY 59 LMEIYEMRELCNGSDCMNDALAEENLKLPRIQNDGCGYGTGNOEICLLKISSGL 118
 DB 61 LEGIALAKREICDKSNMCESSGALAEENLNLPMAKDCQPSGNEETCLKITTTGL 120
 OY 119 EYHSTLEYWKNNLKDKKDKARVLRQRTETLIRFNOEVDLKIYLP 168
 DB 121 EEEVLEYLQNR-ESSKEQAGAVOMSTKGLIOSLOKAKNLISAIPTDP 169

RESULT 11
 O97535 PRELIMINARY; PRT; 160 AA.
 AC O97535;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus vociferans (noisy night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
 RT "Identification, cloning and sequencing of different Interleukin genes
 in 4 Aotus species."
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF014505; AAD01531.1; -
 DR HSSP: P05231; IL6.
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 160 AA: 17855 MW: 07A021338650A46D CRC64;

Query Match 28.0%; Score 307.5; DB 6; Length 160;
 Best Local Similarity 43.6%; Pred. No. 2.5e-19;
 Matches 65; Conservative 30; Mismatches 51; Indels 3; Gaps 3;
 OY 1 MKFLSARDFHPVAF-LGLMLVTTTAPPTSGVRKDFTEDTTPRRPYT-TSGVGLITHV 58
 DB 1 MNSFSTSAFRPAFSLGILLVPAFPVPLGDSKEVAAPRQLTSTEDIDKHIRYI 60
 OY 59 LMEIYEMRELCNGSDCMNDALAEENLKLPRIQNDGCGYGTGNOEICLLKISSGL 118
 DB 61 LEGIALAKREICDKSNMCESSGALAEENLNLPMAKDCQPSGNEETCLKITTTGL 120
 OY 119 EYHSTLEYWKNNLKDKKDKARVLRQRTETLIRFNOEVDLKIYLP 147
 DB 121 EEEVLEYLQNR-ESSKEQAGAVOMSTK 148

RESULT 12
 O9MZ09 PRELIMINARY; PRT; 118 AA.
 AC O9MZ09;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Sylvilagus nuttallii (mountain cottontail).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.
 OX NCBI_TaxID=50378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE-20304414; PubMed-10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 European rabbit (Oryctolagus cuniculus)."
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169178; AAF86662.1; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 118 AA: 13634 MW: 62E97FD3BDEABEC CRC64;

Query Match 18.9%; Score 207.5; DB 6; Length 118;
 Best Local Similarity 36.8%; Pred. No. 8.1e-11;
 Matches 42; Conservative 28; Mismatches 43; Indels 1; Gaps 1;
 OY 97 DCCYOTGYNOEICLLKISSGLLEYHSLYWKNNLKDKKD-KARVLRQRTETLIRFNO 155
 DB 3 DCCFLAANHETCLRTISGLLEFQYVLEHQAQFRSEKENTVSMILKMRHLINVLTP 62
 OY 156 EYKDLKIVLPPIISNALLTKLSQKEMLRTRTQPIKLSLEPFLKYLBSR 209
 DB 63 KYANREGVTLKPAIVASLMDQKQDMKMTTHIFLGLTLPDLPISVR 116

RESULT 13
 O9MZRO PRELIMINARY; PRT; 118 AA.
 AC O9MZRO;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.

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OX NCB1_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Heine H., Delude R.D., Monks B., Golenbock D.T.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044667; AAC02100.1; -
DR HSSP; P05231; 1ALU.
DR InterPro; IPR003573; -
DR Pfam; PF00489; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT NON_TER 101
FT SEQUENCE 101 AA; 11749 MW; 2923BC259CA9A974 CRC64;
SO

Query Match 33.9%; Score 372; DB 11; Length 101;
Best Local Similarity 70.7%; Pred. No. 3.6e-25;
Matches 70; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

OY 93 IORNDGCGTGYNOEICLIKISSGLIEHYSLEYKNNKDKKKARVLRQDTETLIHT 152
DB 2 IORNDGCGTGYNMEICLIKISSGLIDYIYLFETNNVQDKKARVLRQDTETLIHT 61
OY 153 FNOEVKDIHKIVLPTPISNALITDKLESOKEMLRPTKTIO 191
DB 62 FNOEVKDPDKIVMPSPSKAILLEKLESOKMKPRKTIE 100
OY
DB

RESULT 8
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
CN IL-6.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flesippedia; Mustelidae; Enhydra.
OX NCB1_TaxID=14882;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schenkel M.D., McKnight M.L., Reiderman T.H., Hanni K.D.,
RA Stolt J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL EMBL; I46804; AA01428.1; -
DR HSSP; P05231; IL6.
DR InterPro; IPR003573; -
DR InterPro; IPR003574; -
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFNGF.
DR PROSITE; PS00254; INTERLEUKIN_6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT NON_TER 101
FT SEQUENCE 207 AA; 23527 MW; 729EB0CD91136DBB CRC64;
SO

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Query Match 33.1%; Score 363.5; DB 6; Length 207;
Best Local Similarity 38.8%; Pred. No. 4.6e-24;
Matches 81; Conservative 48; Mismatches 71; Indels 9; Gaps 5;

OY 5 SARPEHPVAF-IGLMLVTTTAPTSOVRGDEDTTPNRPVYTTTS-OVGGLITHVIMEI 62
DB 2 STSAPSVAVSLGLLVMATAPFTPPGLGDSKDATSNRPPLISADKMEFIFILGKI 61
OY 63 VEMKELCNGNSDCMNDALAEENNLKLPETQIRNDGCGTGYNOEICLIKISSGLIEHYS 122

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DB 62 SALRNEKCDKYNKCEDESKVELAENNLNPKLAEKRCOSRFPNOETCLITTTGLDGFQI 121
OY 123 YLEYKNNLKNKKDKARVLRQDTETLIHIFNOEYKDLAKT-VLPTPISNALITDKLES 180
DB 122 HLKYLIESNYEGN-KDNAHSYVYSTKHLT---QTLRPANQIEVTPPTDASIALQFKS 176
OY 181 OKEMLRPTKTIOFLKSLIEFLVYLRSTR 209
DB 177 QDKWLKTTTHLLRLRLEDFLOFSRLAIR 205

RESULT 9
ID Q9MZRL PRELIMINARY; PRT; 241 AA.
AC Q9MZRL;
DC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN 6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCB1_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=SPLEEN, LYMPH NODE;
RA MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytochrome 12:555-565(2000).
DR EMBL; AF169176; AAF86660.1; -
DR InterPro; IPR003573; -
DR InterPro; IPR003574; -
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFNGF.
DR PROSITE; PS00254; INTERLEUKIN_6.
DR PROSITE; PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART; SM00126; IL6; 1.
FT SEQUENCE 241 AA; 27021 MW; 781D323692C3EE97 CRC64;
SO

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Query Match 31.0%; Score 340.5; DB 6; Length 241;
Best Local Similarity 36.6%; Pred. No. 5.4e-22;
Matches 71; Conservative 42; Mismatches 80; Indels 1; Gaps 1;

OY 15 IGLMLVTTTAPTSOVRGDEDTTPNRPVYTTTS-OVGGLITHVIMEIEMKELCNGNS 74
DB 17 LALLLVATATFPISAPVREDSNKKASPDKTLRPPGTIRLSIRSLIEFKELKRCMDCHV 76
OY 75 DCANNDALAEENNLKLPETQIRNDGCGTGYNOEICLIKISSGLIEHYSLEYKNNIK-D 133
DB 77 NCMNRKALAEVNLKLPRLLEEDGCPPAVNNETILRTSGLMEFRVYLEHLOAKPRSD 136
OY 134 NKKDKARVLRQDTETLIHIFNOEYKDLAKT-VLPTPISNALITDKLESOKEMLRPTKTIOFI 193
DB 137 EENRVSVMVLKNQIHLKTLRPAVKVNLNEATLKPAVAVSLMENLOKNOGLKTTTHFI 196
OY 194 LKSLIEFLVYLRSTR 207
DB 197 LKGLTNFLEFTLRA 210

RESULT 10
ID Q9TH4 PRELIMINARY; PRT; 175 AA.
AC Q9TH4;
DC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
CN IL-6.

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Db 61 IYELRRELCLNNNGCHNDNDVLLNNELPVIQINDGCLQTYNMEICLKITSGLLDYQ 120
 QY 122 SYLEYMKNNKDKKKRKYARVQDRTELLIHINQEVKOLHKIVLPTPISNALLTDKLEQ 181
 Db 121 IYEFVFNNAVQDKKKRKYARVQDRTELLIHINQEVKOLHKIVLPTPISNALLTDKLEQ 180
 QY 182 KEMRLRTKTIQFIILKSLEEFKLVLTASTRO 210
 Db 181 KEMRLRTKTIQFIILKSLEEFKLVLTASTRO 209

RESULT 2
 Q9JHH3 PRELIMINARY; PRT; 207 AA.
 AC Q9JHH3;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
 OC Marmota.
 OC NCBI_Taxid=995;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA Li D.H., Cullen J.M.;
 RT "The Woodchuck Interleukin-6 Gene : Cloning and Structural Analysis.";
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li D.H., Cullen J.M.;
 RT "Gene Structure of the Woodchuck Interleukin-6.";
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF012808; AAF34861.1; -;
 DR EMBL: AF12896; AAF28873.1; -;
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PRO0433; IL6GCSFWGF.
 DR PRINTS: PRO0434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA; 23645 MW; AD2F46E450E13470 CRC64;

Query Match 44.0%; Score 483; DB 11; Length 207;
 Best Local Similarity 44.8%; Pred. No. 2e-34;
 Matches 95; Conservative 47; Mismatches 62; Indels 8; Gaps 3;

QY 1 MKFLSADPFRVAFGLIMLYTTTAPTSQVRGDFTEDTTPNRVYTTTS-OVGLLTHVL 59
 Db 1 MKFPS-----IASLGLLVAVAFAPASLOREDGNSVTRKRPTRASGKTAQIYLI 54
 QY 60 WEIYEMRKELCNGNSDCMNNDDALAENNLKLPETIORNDGCVOTGYNOEICLKISSGLLE 119
 Db 55 KEVEYEMRKELCKNDGTCISHVAVSNNLNLPKMTKXGSCQOTGYNRRNCIVRTSGILE 114
 QY 120 YHSLEYMKNNKLD-KKKDKARYLQDTELLIHINQEVKOLHKIVLPTPISNALLTDKL 178
 Db 115 FOYLRVYIRKPFQGNRRDAFHVQSSKALIEILKQEVKPNKLVPSPIANINLAKL 174
 QY 179 ESQKEMLRKTIQFIILKSLEEFKLVLTASTRO 210
 Db 175 ESQNDQKQVMTMOLISNEDFLOPTLBAVRK 206

RESULT 3
 Q97340 PRELIMINARY; PRT; 209 AA.
 ID Q97340;
 AN Q97340;

DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus nancymae (owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_Taxid=37293;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Echeverry S.J., Hernandez E., Moreno A., Patatroyo M.E., Murillo L.A.;
 RT "Identification, cloning and sequencing of different Interleukin genes
 in 4 Aotus species.";
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF014510; AAD01536.1; -;
 DR HSSP: P05231; 1ALU;
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PRO0433; IL6GCSFWGF.
 DR PRINTS: PRO0434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR NON_TER 1
 FT NON_TER 1
 FT SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 38.9%; Score 427.5; DB 6; Length 209;
 Best Local Similarity 42.6%; Pred. No. 1.3e-29;
 Matches 89; Conservative 43; Mismatches 74; Indels 3; Gaps 3;

QY 1 MKFLSADPFRVAFGLIMLYTTTAPTSQVRGDFTEDTTPNR-PYTTSQVGLLTHV 58
 Db 1 MNSFSTAFRPAFASGLLLVMPAPFAPVPGEDSKVAAVRQPLTSTQIDKRIYI 60
 QY 59 LMEIYEMRKELCNGNSDCMNNDDALAENNLKLPETIORNDGCVOTGYNOEICLKISSGL 118
 Db 61 LDGIALRKELCKNSNNCESSKALAFNNLNPKMAEKDGCQSFNEETCLVITIGLL 120
 QY 119 EYHSLEYMKNNKDKKKRKYARVQDRTELLIHINQEVKOLHKIVLPTPISNALLTDKL 178
 Db 121 EFEYLEYLQNR-ESSEQARVAVQSTVYLQFLOKRAKKNLDAITTPPTNSSLTKL 179
 QY 179 ESQKEMLRKTIQFIILKSLEEFKLVLTASTRO 207
 Db 180 QANQMLQDMTHLILRSFKFLOSSLRA 208

RESULT 4
 Q9XT80 PRELIMINARY; PRT; 208 AA.
 AC Q9XT80;
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
 DE INTERLEUKIN 6 PRECURSOR
 OS Delphinapterus leucas (Beluga whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodontidae; Delphinapterus.
 OC NCBI_Taxid=9749;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
 RT "Molecular cloning and phylogenetic analysis of Beluga whale
 (Delphinapterus leucas) Interleukin 6.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF076643; AAD42929.1; -;
 DR HSSP: P05231; 1ALU;
 DR SMART: SM003573; -;
 DR InterPro: IPR003574; -;

OM protein - protein search, using SW model
Run on: October 4, 2001, 19:12:00

Run on: October 4, 2001, 19:12:00 ; Search time 74.43 seconds
(without alignments)
375.069 Million cell updates/sec

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Title: US-09-230-048-4
Perfect score: 1098
Sequence: 1 MFLSARDHPVAFGLMLV.....FLKSLPEEPKVTLRSTROT 2111

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Scoring table: BIOSUM62

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum Match 1008
Listing first 45 summaries

Datatabse

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1:  sp.archaea: *
2:  sp.bacteria: *
3:  sp.fungi: *
4:  sp.human: *
5:  sp.invertebrate: *
6:  sp.mammal: *
7:  sp.mhc: *
8:  sp.organelle: *
9:  sp.phage: *
10: sp.plant: *
11: sp.podent: *
12: sp.unclassified: *
13: sp.veterebrate: *
14: sp.virus: *

```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	774.5	70.5	210	11	Q9WV08	Q9WV08 mesocricetus
2	483	44.0	207	11	Q9JHH3	Q9JHH3 marmota mon
3	427.5	38.9	209	6	Q9J540	Q9J540 actus nancy
4	420	38.3	208	6	Q9XTH80	Q9XTH80 delphinus
5	411.5	37.5	209	6	Q9PTT83	Q9PTH3 actus lemur
6	402	36.6	207	6	Q9MY27	Q9MY27 canis famill
7	372	33.9	201	11	Q505041	Q505041 ericeetus
8	363.5	33.1	207	6	Q28403	Q28403 embryda lut
9	340.5	31.0	241	6	Q9M4R1	Q9M4R1 oryctolagus
10	336.5	30.6	175	6	Q9TTH4	Q9TTH4 actus nigri
11	307.5	28.0	160	6	Q9J535	Q9J535 actus vocif
12	207.5	18.9	118	6	Q9M209	Q9M209 sylvaiaqus
13	205.5	18.7	118	6	Q9M2R0	Q9M2R0 sylvaiaqus
14	199.5	18.2	118	6	Q9M208	Q9M208 lepus colif
15	199.5	18.2	115	6	Q9M205	Q9M207 lepus townsi
16	193.5	18.2	115	6	Q9M205	Q9M205 oryctolagus
17	150	13.7	204	14	Q40918	Q40918 kaposi's sa
18	148	13.5	204	6	Q98823	Q98823 kaposi's sa
19	147.5	13.4	94	6	Q627785	Q627785 felis silve

20	103	9.4	977	09U0H9	09U0H9 plasmodium
21	96	8.7	196	11	09EO14
22	98	8.7	819	5	093228
23	95	8.7	325	14	091879
24	95	8.7	342	14	09EBN3
25	93.5	8.5	1554	6	077819
26	90.5	8.2	1127	14	09VVT6
27	90.5	8.2	2742	5	025766
28	98.5	8.1	553	5	09VKR2
29	88.5	8.1	826	5	09N894
30	88	8.0	421	10	09LX20
31	87.5	8.0	643	5	09V4C1
32	87	7.9	421	10	P92952
33	86.5	7.9	480	10	09SH00
34	86.5	7.9	645	2	007869
35	86.5	7.9	743	10	09ZVX5
36	86.5	7.9	768	5	09NAK6
37	86.5	7.9	823	4	09H016
38	85.5	7.8	1516	5	096154
39	85	7.7	189	4	09H2A5
40	85	7.7	1098	8	09RZW8
41	85	7.7	2771	5	026216
42	84.5	7.7	207	14	09EMR7
43	84.5	7.7	1156	2	066878
44	84	7.7	189	4	09NPF7
45	84	7.7	636	2	051624
					09U0H9 plasmodium
					09eq14 mus musculi
					093228 caenorhabdl
					091b3 turkey herfr
					096b3 turkey herfr
					077819 oryctolegus
					09vvt6 melanoplus
					025766 plasmodium
					09vkr2 dtrosophila
					09n894 plasmodium
					09lkr20 arabiopsis
					09v4c1 dtrosophila
					p92952 arabiopsis
					09shq0 arabiopsis
					007869 streptococ
					09rvx5 arabiopsis
					09nak6 dictyostell
					09h016 homo saplen
					096154 plasmodium
					09h2a5 homo saplen
					09rzw8 borellia bu
					026216 plasmodium
					09emr7 annecta moc
					066878 aguilax aeo
					09npf7 homo saplen
					051624 borellia bu

ALIGNMENTS

RESULT	1			
09WV08		PRELIMINARY;	PRT;	210 AA.
ID	09WV08			
AC	09WV08;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	IL-6 (FRAGMENT).			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_Taxid=10036;			
IN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRATN-APA; TISSUE=KIDNEY;			
RC	RA			
RT	Nishida E.;			
RL	"APA hamsters IL-6 partial cDNA."			
DR	Submitted (TUN-1989) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AB028635; BAA/8766.1; -.			
DR	HSSP; P05231; 1ALU.			
DR	Interpro; IPR003573; -.			
DR	Interpro; IPR003574; -.			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GSGFMGF.			
DR	PRINTS; PR00434; INTERLEUKIN6.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
DR	SMART; SM00126; IL6; 1.			
FT	NON_TER			
FT	1			
FT	1			
Q	SEQUENCE 210 AA: 24060 MW: 269319AFBB913AB3 CRC64;			

Query Match	70.5%;	Score 774.5;	DB 11;	Length 210;
Best Local Similarity	72.7%;	Pred. No. 1e-59;		
Matches 152;	Conservative 22;	Mismatches 34;	Indels 1;	Gaps 1

0y 3 FL SARDFH FVA LGLMLVT TTA APT SQVRKGD PTD ETT PRRPYTTS -QVGLLTHVME 61
1 FL SARDFH FPLVFLGL LLMVAVALPT SQVRKGD PTD ETT PRRPYTTS QGVGLTVYLR 60
62 IYMRKELCNGSDCHNDDLAENNIKLPEIQKNGCIVOTGINDICLLKISSLLEYH 122


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CC -----
CC EMBL: L26028; AAA9978.1;
CC HSSP: P05231; 1A1U.
CC InterPro: IPR001716;
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6CSPMGF.
CC PROSITE: PS00254; INTERLEUKIN-6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29
CC CHAIN 30 212
CC DISULFID 72 78
CC DISULFID 101 111
CC CARBOHYD 73 73
CC CARBOHYD 172 172
CC SEQUENCE 212 AA; 23728 MW; 4130FE0CF0BCAD CRC64;

Query Match 37.5%; Score 411.5; DB 1; Length 212;
Best Local Similarity 40.1%; Pred. No. 3e-27;
Matches 85; Conservative 48; Mismatches 76; Indels 3; Gaps 3;

OY 1 MKFLSARDHPVAF-IGLMVTTTAPPTSOVARGDFTEDTP-NRPVYTSQVGLITHV 58
DB 1 MNSFSTSAFGPAFSLGILLVPAFPAVLPGEDSKVAPHSOPLTSERIORKHRYI 60
OY 59 LWEIVEMRKELNGNSDCNNNDALAEENLKLPETQRNDGCGYGTGNOECLIKISSGL 118
DB 61 LDGISAIRKFKCRSMCESSKEALAEENNLKPKAEKDGFGSGFNEEDCLVITIGLL 120
OY 119 EYHSYLEYMKNNKDKKKARVLDQTEFTLHIFNDEVKDLKIVLPPTISNALLTDKL 178
DB 121 EFVEYLEYLONRF-ESSEQARAYOMSTKVLIQFLOKKAKMLDITTPPTNASLTKL 179
OY 179 ESQEWLRTKTIOFILKSLEEFKAVTLRSTRO 210
DB 180 QANOMLQDMWTHILTLRSFKERFLQSNLRAHQ 211

RESULT 15
IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=94162386; PubMed=8117820;
RA Bradley W.G., Gibbs C., Kraus V., Good R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline
interleukin-6."
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----
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CC -----
CC EMBL: L16914; AAA1660.1;
CC HSSP: P05231; 21L6.
CC InterPro: IPR001716;
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6CSPMGF.
CC PROSITE: PS00254; INTERLEUKIN-6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 27
CC CHAIN 28 208
CC DISULFID 68 74
CC DISULFID 97 107
CC CONFLICT 2 2
CC CONFLICT 45 45
CC CONFLICT 133 133
CC CONFLICT 173 187
CC CONFLICT 200 201
CC SEQUENCE 208 AA; 23401 MW; 93B4456B2989CAAC CRC64;

Query Match 36.6%; Score 401.5; DB 1; Length 208;
Best Local Similarity 38.9%; Pred. No. 2e-26;
Matches 82; Conservative 51; Mismatches 71; Indels 7; Gaps 4;

OY 1 MKFLSARDHPVAF-IGLMVTTTAPPTSOVARGDFTEDTPNR-PVYTSQVGLITHV 58
DB 1 MFLSTSAFSPAFSLGILLVVAFAFPP-GLGSDATSNLPLTSADKKEELIKYI 56
OY 59 LWEIVEMRKELNGNSDCNNNDALAEENLKLPETQRNDGCGYGTGNOECLIKISSGL 118
DB 57 LKISALKKEMCMQNYKCDSEKALAEENNLKPKAEKDGFGSGFNEEDCLVITIGLL 116
OY 119 EYHSYLEYMKNNKDKKKARVLDQTEFTLHIFNDEVKDLKIVLPPTISNALLTDKL 178
DB 117 EFQYLYLEFDKY-ESDENNAKSVYTSNVILLQMLKRGKNQDEVITPVTVEVGLQAKL 175
OY 179 ESQEWLRTKTIOFILKSLEEFKAVTLRSTR 209
DB 176 OSQEWLRTKTIOFILKSLEEFKAVTLRSTR 206

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Search completed: October 4, 2001, 19:12:35
Job time: 270 sec

Fri Oct 5 10:02:18 2001

DR HSP: P05231; IL6.
DR Interpro: IPR001716; -
DR Pfam: PF004489; IL6; 1
DR PRINTS: PR00433; IL6GSPMGF
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; signal.
FT SIGNAL 1 29
FT CHAIN 30 212
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT CARBOHYD 172 172
SQ SEQUENCE 212 AA: 23668 MW: 730035226B4B9P CRC64;

Query Match 37.8%; Score 414.5; DB 1; Length 212;
Best Local Similarity 40.1%; Pred. No. 1.7e-27;
Matches 85; Conservative 50; Mismatches 74; Indels 3; Gaps 3;

OY 1 MKETISANDPPIPAF-LGLMLVTTTAPPTSOVRGDEFTDTP-NRPVYTTQVGLITHV 58
Db 1 MNSESTAFGVAFSLGLLVLPAPVLPGEDESKVAVAFHSQPLTSERIRKHRYI 60
OY 59 LMEIVENKEICNGSDCMNDALAEENIKLPEIORNDGCVOTGYNOEICLLKISSGL 118
Db 61 LDGIALRKETCRNSMCDSTKALAEENLPRKAEKDCQSGFNDCTLVYITIGLL 120
OY 119 EYHYLEYKMKNLKDKKARVLRQDTETLIHIFNOEYKDLIKIVLPISNALLTDKL 178
Db 121 EYVYLYLQNR-ESSEEQARAVQSTKVLQLQLOKAKKNDAITVPEPTNASTLTKL 179
OY 179 ESQKEMLRITIOILKSLSEFLKVTLRSTRQ 210
Db 180 QAGNQWLDWMTLILRSFREFQSSLRALRQ 211

RESULT 13
IL6_PROV1 STANDARD; PRT: 209 AA.
ID IL6_PROV1
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Planipectia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Redarson T.H., Hanni K.D.,
STOET J.L., Verrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nevels).";
RT Immunogenetics 43:190-195(1996).
RL

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC EMBL: L46802; AB01430.1; -
CC DR HSP: P05231; IL6.
CC DR Interpro: IPR001716; -
CC DR Pfam: PF004489; IL6; 1.
CC DR PROSITE: PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; signal.
FT SIGNAL 1 26
FT CHAIN 27 209
FT DISULFID 69 75
FT DISULFID 98 108
SQ SEQUENCE 209 AA: 23483 MW: 75144922643B4B9P CRC64;

Query Match 37.7%; Score 413.5; DB 1; Length 209;
Best Local Similarity 41.4%; Pred. No. 2e-27;
Matches 87; Conservative 51; Mismatches 67; Indels 5; Gaps 4;

OY 2 KFLSARDPPIPAF-LGLMLVTTTAPPTSOVRGDEFTDTPNRPVYTT-SQVGLITHV 59
Db 1 RFTSA-FSPVAFSLGLLVMTATPPTPGVGEQVATSNRPPTSPOKMEEFIVYL 58
OY 60 WEIVEMKEICNGSDCMNDALAEENIKLPEIORNDGCVOTGYNOEICLLKISSGL 119
Db 59 GKISALRKEMCDKYNKCEDSKALAEENLPRKAEKDCQSGFNDCTLVYITIGLE 118
OY 120 YHYLEYKMKNLKDKKARVLRQDTETLIHIFNOEYKDLIKIVLPISNALLTDKLE 179
Db 119 FOHAKTYOANVECKNED-ANSVISTKLQVQIMKKVKSQDEVTTPPTDTSLOALIK 177
OY 180 SOKEMLRITIOILKSLSEFLKVTLRSTR 209
Db 178 AQRKWLKHTIHLILNSLEDLQFSLRVR 207

RESULT 14
IL6_MACMU STANDARD; PRT: 212 AA.
ID IL6_MACMU
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RAC 2;
RA MEDLINE=96003435; PubMed=7561102;
RA Vulliamer F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates";
RT J. Immunol. 155:3946-3954(1995).
RL

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC *****
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DR PRINTS: PR00433; IL6GSPMGF.
DR PRINTS: PR00434; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC96GCI3E3230A0 CRC64;

Query Match 38.2%; Score 419.5; DB 1; Length 208;
Best Local Similarity 40.8%; Pred. No. 6,5e-28;
Matches 86; Conservative 47; Mismatches 71; Indels 7; Gaps 4;

OY 1 MKFLSADDFPVAF-LGLMLVTTTAPPTSOVARQDFTDTP-NRPVYTT-SQVGGLTTHV 58
DB 1 MNSVTSAPFSPVAFSGLLVLPAPFAPVLPGEDESKVAAHPQPTSSERIDKHRTI 60
OY 59 LMEIYERKKELCNGNSDCMNDALAEENLKLPEIQRNDGCGYGTQNOEICLKISSGL 118
DB 61 LDGISAIRKKEICERKNDCEKSKETLAEENLKLPEKEDGCGFGSFGNATCLITTTGGL 120
OY 119 EYHSLEYMKNNLKDKKKARVLODTELTLIHINQYKDLKIVLPTPSNALLTDKL 178
DB 121 EYQYLYDFIQNEFEGN-QETVMELOSISRTLIQILKEIKAGL---IYTPATHMDLMEK 175
OY 179 ESQKEMLRKTIOFILKSLEEFLLKTVLRSTR 209
DB 176 QSNENWKNKAKVILLIRSLLENFLQFSLRAIR 206

RESULT 11
ID IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOID AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000554; BA019148.1; -
CC HSSP; P05231; 21L6.
CC InterPro; IPR001716; -

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DR Pfam: PR00489; IL6; 1.
DR PRINTS: PR00433; IL6GSPMGF.
DR PRINTS: PR00434; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CFB173FCHFB080389 CRC64;

Query Match 37.8%; Score 415.5; DB 1; Length 212;
Best Local Similarity 40.1%; Pred. No. 1,4e-27;
Matches 85; Conservative 51; Mismatches 73; Indels 3; Gaps 3;

OY 1 MKFLSADDFPVAF-LGLMLVTTTAPPTSOVARQDFTDTP-NRPVYTT-SQVGGLTTHV 58
DB 1 MNSVTSAPFSPVAFSGLLVLPAPFAPVLPGEDESKVAAHPQPTSSERIDKHRTI 60
OY 59 LMEIYERKKELCNGNSDCMNDALAEENLKLPEIQRNDGCGYGTQNOEICLKISSGL 118
DB 61 LDGISAIRKKEICERKNSMCCSKKALAEENLKLPEKEDGCGFGSFGNEDICVKTITGL 120
OY 119 EYHSLEYMKNNLKDKKKARVLODTELTLIHINQYKDLKIVLPTPSNALLTDKL 178
DB 121 EYQYLYDFIQNRF-ESSEQDARAVOSTKVLQFLQKRAKMLDAITPEPTNASLITKL 179
OY 179 ESQKEMLRKTIOFILKSLEEFLLKTVLRSTRQ 210
DB 180 QAQNMQDMTTHLILRSFREFLOSLRALRQ 211

RESULT 12
ID IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RL MEDLINE=96003435; PubMed=7561102;
CC *Comparative sequence analysis of cytokine genes from human and
CC nonhuman primates.*
CC J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOID AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL; L26032; AAA99972.1; -

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Query Match
Best Local Similarity 41.8%; Pred. No. 5.5e-26;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

38.3%; Score 420.5; DB 1; Length 212;

1 MKFLSARDHPVAF-LGLMLVTTAFTPTSOVRKQDPTED--TPPNR-PVYTTSOVGGLIYH 57
1 MNSFSTSAFGPAFSLGLLVLPAAP-APVPGEDSKDVAAPHROPLTSSERIDKQIRY 59
58 VLMETVAREKRELCNGNSCMNDALAEENNLKLPRIQRNDGCGYQGYNOEICLKISSGL 117
60 LIDGIALKREKCNKSNKSSKEALAEENNLKPKMAEKDCGCGFNGEITGLVYQIYDLYONE- 119
118 LEYHSLLEYKMNKNLKNKDKARVLRDTEFLIHFNQEVKDLKIVLPPTISNALLTDR 177
120 LFEFYYLEYLRNF-ESSEEDQARAQWSTFVLLQFLQKKAKINDAITPDPPTNASLLTK 178
178 LESOKEMLRRTKTFQFLKSLPEFLKVTLRSTR 210
179 LQANQNMQDNTLILSLILSLFKFELQSSLRALRQ 211

RESULT 9
116_ORCOR
ID IL6_ORCOR STANDARD PRT; 205 AA.
AC 028747:
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OC NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
Stoct J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of Interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), Killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL: L46803; AB01429.1; -
DR HSSP: P05231; IL6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT NON_TER 1
FT CHAIN 21
FT CHAIN 22 205 BY SIMILARITY.
FT DISULFID 64 70 INTERLEUKIN-6.
FT DISULFID 93 103 BY SIMILARITY.

FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 205 AA; 23266 MW; 6308BP34457960832 CRC64;

Query Match
Best Local Similarity 43.9%; Pred. No. 6.4e-28;
Matches 87; Conservative 42; Mismatches 64; Indels 5; Gaps 4;

38.2%; Score 419.5; DB 1; Length 205;

15 LGLMLVTTAFTPTSOVRKQDPTEDTPPNRPVYTTS--QVGLLTHVLMETVAREKRELCNG 72
8 LGLMLVTTAFTPTSOVRKQDPTEDTPPNRPVYTTS--QVGLLTHVLMETVAREKRELCNG 66
73 NSDCMNDALAEENNLKLPRIQRNDGCGYQGYNOEICLKISSGLLEYHSLLEYKMNLIK 132
67 YKCEKSKKALAEENNLKPKMAEKDCGCGFNGEITGLVYQIYDLYONE- 125
133 DNKKDKARVLRDTEFLIHFNQEVKDLKIVLPPTISNALLTDRKLESOK-EMLRRTKQ 191
126 EDDKKEIAEVQSSKALAQILRKQVKNPDEVYTPDPPTNASLNNLQSDNDMMKNTKLI 185
192 FLKSLPEFLKVTLRSTR 209
186 LILRSLENTLQFSLRAIR 203

RESULT 10
IL6_SHEEP
ID IL6_SHEEP STANDARD PRT; 208 AA.
AC P29453:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E., Batcham G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
Nash A.D.;
RT "Molecular cloning and characterization of a ruminant interleukin-6
cDNA.";
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ebrahimi B.;
RL Submitted (OCT-1992) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: X62501; CAA44363.1; -
DR EMBL: X68723; CAA48662.1; -
DR EMBL: A19159; CAA01443.1; -
DR FIR: S29349; S29349.
DR HSSP: P05231; IL6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.


```

OY 1 MKPLSARDHPVAF-LGIMLVTTTAPPTSOVRRGDEPTEDTPNRPVYTT-SOVGGLITHV 58
DB 1 MNSLSTAFSPVAFSGLLLVMTATPPTGRLSEDAKGDATSDKMLFTSPKTELLIKYI 60
OY 59 LMEIVEMRKELCNGSDCNNDALAEENNLKLPETIORNDGCYOTGYNOELICLISGGL 118
DB 61 LKISAPRKEICEKCEYENKSEKSEVLAENNLNLPKMAEKCEGFCOSGFOENOTIMITGLV 120
OY 119 EYHSYLEYMKNNKDKKARVLODTEFLIHFNQEVKDLHKVLPTPISNLLTDKL 178
DB 121 EFOIYLDLQKEFESN-KGVNEAVOISTKALLIOTLRKOKKNPDKATTPNTMAGLDKL 179
OY 179 ESQREMLRTKTIOTFIKLSLEELKVTLRSTR 209
DB 180 OSQNEWMKNTKRIILIRLESDFLQFSLRAIR 210

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RESULT 5

IL6_CAPHL. STANDARD: PRT: 208 AA.

```

AC Q28319: 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_Taxid=9925;
RN [1]
RX MEDLINE-97392354: PubMed-9250586;
RT Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells.";
RT Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL: D86569; BAA1318.1; -
CC DR HSSP; P05231; 21L6.
CC DR InterPro; IPR001716; -
CC DR Pfam; PF00489; IL6; 1.
CC DR PRINTS; PRO0433; IL6GSPMGF.
CC DR PRINTS; PRO0434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN6; 1.
CC KM Cytokine; Glycoprotein; Growth factor; Signal.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1
CC FT CHAIN 1
CC FT SIGNAL 29
CC FT CHAIN 30
CC FT DISULFID 72
CC FT DISULFID 78
CC FT DISULFID 101
CC FT CARBOHYD 38
CC FT CARBOHYD 38
CC SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

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OY 1 MKPLSARDHPVAF-LGIMLVTTTAPPTSOVRRGDEPTEDTPNRPVYTT-SOVGGLITHV 58
DB 1 MNSLSTAFSPVAFSGLLLVMTATPPTGRLSEDAKGDATSDKMLFTSPKTELLIKYI 60
OY 59 LMEIVEMRKELCNGSDCNNDALAEENNLKLPETIORNDGCYOTGYNOELICLISGGL 118
DB 61 LKISAPRKEICEKCEYENKSEKSEVLAENNLNLPKMAEKCEGFCOSGFOENOTIMITGLV 120
OY 119 EYHSYLEYMKNNKDKKARVLODTEFLIHFNQEVKDLHKVLPTPISNLLTDKL 178
DB 121 EFOIYLDLQKEFESN-KGVNEAVOISTKALLIOTLRKOKKNPDKATTPNTMAGLDKL 179
OY 179 ESQREMLRTKTIOTFIKLSLEELKVTLRSTR 209
DB 176 OSQNEWMKNTKRIILIRLESDFLQFSLRAIR 206

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RESULT 6

IL6_BOVIN STANDARD: PRT: 208 AA.

```

AC P26892: 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RX MEDLINE-93076003: PubMed-1446077;
RT Droogmans L., Cluets I., Cleuter Y., Kettmann R., Burny A.;
RT "Nucleotide sequence of bovine Interleukin-6 cDNA.";
RT DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL: X57317; CAA40572.1; -
CC DR PIR; S22162; S22162.
CC DR HSSP; P05231; 21L6.
CC DR InterPro; IPR001716; -
CC DR Pfam; PF00489; IL6; 1.
CC DR PRINTS; PRO0433; IL6GSPMGF.
CC DR PRINTS; PRO0434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN6; 1.
CC KM Cytokine; Glycoprotein; Growth factor; Signal.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1
CC FT CHAIN 1
CC FT SIGNAL 29
CC FT CHAIN 30
CC FT DISULFID 72
CC FT DISULFID 78
CC FT DISULFID 101
CC FT CARBOHYD 38
CC FT CARBOHYD 38
CC SEQUENCE 208 AA; 23758 MW; A0F00B9BA2EC341 CRC64;

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Query Match 38.7%; Score 424.5; DB 1; Length 208;
 Best Local Similarity 41.2%; Pred. No. 2.5e-28;
 Matches 87; Conservative 46; Mismatches 71; Indels 7; Gaps 4;

Query Match 38.5%; Score 422.5; DB 1; Length 208;
 Best Local Similarity 42.4%; Pred. No. 3.7e-28;
 Matches 89; Conservative 46; Mismatches 66; Indels 9; Gaps 5;


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RT "DNA rearrangement and constitutive expression of the interleukin 6
RT gene in a mouse plasmacytoma.";
RL J. Exp. Med. 171:965-970(1990).
RN
RP SEQUENCE OF 25-211;
RX MEDLINE-88329059; PubMed-3262059;
RX Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
RX "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
RX sequence and relation to human interleukin-6.";
RL Eur. J. Biochem. 176:187-197(1988).
RN
RP SEQUENCE OF 66-75; 78-84 AND 128-148.
RX MEDLINE-90147691; PubMed-2302197;
RX Jahnes W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
RX "Internal amino acid sequencing of proteins by in situ cyanogen
RX bromide cleavage in polyacrylamide gels.";
RL Biochem. Biophys. Res. Commun. 166:139-145(1990).
RN
RP SEQUENCE OF 25-45.
RX MEDLINE-87092311; PubMed-2948184;
RX van Snick J., Cayphas S., Yank A., Uytendhoeve C., Coulle P.G.,
RX Rubira M.R., Simpson R.J.;
RX "Purification and NH2-terminal amino acid sequence of a
RX T-cell-derived lymphokine with growth factor activity for B-cell
RX hybridomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X06203; CAA29560.1; -
DR EMBL: M20572; AAA39302.1; -
DR EMBL: X51457; CAA35824.1; -
DR EMBL: J03783; AAA39301.1; -
DR EMBL: X54542; CAA38411.1; -
DR EMBL: M24221; AAA68814.1; -
DR PIR: A30531; ICMS6.
DR HSSP: P05231; 1ALU.
DR MGD: MGI:96559; IL6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6CSFNGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
DR CYCLOP: Growth factor; Glycoprotein; Signal.
KM SIGNAL 1 24
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SO SEQUENCE 211 AA: 24384 MW: 88470 DA:9E86787A CAC64;

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Query Match 100.0%; Score 1098; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 6; Be-84;
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QY 61 EIVEMKRELNGNSDCNNDDALAENNLKLPETIORNDGCYOTGNOEICLKISSGLEY 120

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DB 61 EIVEMKRELNGNSDCNNDDALAENNLKLPETIORNDGCYOTGNOEICLKISSGLEY 120
QY 121 HSYLEVKNKNNKDKKKARVLOQDTELIHIFNOEYKDLKIVLPPIPSNALLTDKLES 180
DB 121 HSYLEVKNKNNKDKKKARVLOQDTELIHIFNOEYKDLKIVLPPIPSNALLTDKLES 180
QY 181 QKEWLRRTKTIQFIKSLSEEFKATLSTROT 211
DB 181 QKEWLRRTKTIQFIKSLSEEFKATLSTROT 211

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RESULT 2

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ID IL6_RAT STANDARD; PRT; 211 AA.
AC P20607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89380206; PubMed-2789217;
RX Northmann W., Braciak T.A., Hattori M., Lee F., Fey G.H.;
RX "Structure of the rat interleukin 6 gene and its expression in
RX macrophage-derived cells.";
RL J. Biol. Chem. 264:16072-16082(1989).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M26744; AAA77659.1; -
DR EMBL: M26745; AAA41430.1; -
DR PIR: A34247; A34247.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6CSFNGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6; 1.
DR CYCLOP: Growth factor; Glycoprotein; Signal.
KM SIGNAL 1 24
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SO SEQUENCE 211 AA: 24357 MW: 17024814 F96B5C1 CAC64;

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Query Match 86.0%; Score 944; DB 1; Length 211;
 Best Local Similarity 85.3%; Pred. No. 3; Se-71;
 Matches 180; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MKPLSARDHFVAFGLMLVTTAFPTSOVRGDFEDTTPRPVYTTSOVGGILITVLM 60
DB 1 MKPLSARDHFVAFGLMLVTTAFPTSOVRGDFEDTTPRPVYTTSOVGGILITVLM 60
QY 61 EIVEMKRELNGNSDCNNDDALAENNLKLPETIORNDGCYOTGNOEICLKISSGLEY 120

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GenCore version 4.5
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Om protein - protein search, using sw model

Run on: October 4, 2001, 19:12:34 ; Search time 27.34 Seconds

(without alignments)
264,371 Million cell updates/sec

Title: US-09-230-048-4

Perfect score: 1098
Sequence: 1 MKFLSARDPHRYAFLGLMLV.....PIIKSLREPLKWTINSTROP 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1098	100.0	1 IL6_MOUSE	P08505 mus musculus
2	944	86.0	1 IL6_RAT	P20607 rattus norv
3	475	43.3	1 IL6_MARMO	O35736 marmota mon
4	428.5	39.0	1 IL6_PIG	P26893 sus scrofa
5	424.5	38.7	1 IL6_CAPI	O28313 capra hircu
6	423.5	38.5	1 IL6_BOVIN	P26892 bos taurus
7	420.5	38.3	1 IL6_HORSE	O35181 equus caball
8	420.5	38.3	1 IL6_HUMAN	P05231 homo sapien
9	419.5	38.2	1 IL6_ORCOR	O28747 orctinus orc
10	419.5	38.2	1 IL6_SHEEP	P29455 ovis aries
11	415.5	37.8	1 IL6_MACFA	P79341 macaca fasc
12	414.5	37.8	1 IL6_CERTO	P46650 cercocebus
13	413.5	37.7	1 IL6_PHOVI	O28819 phoca vitul
14	411.5	37.5	1 IL6_MACMU	P51494 macaca mula
15	401.5	36.6	1 IL6_PELCA	P41688 felis silve
16	386	35.2	1 IL6_CANFA	P41323 canis fami
17	229.5	20.9	1 IL6_MUSVI	P41693 mustela vis
18	95	8.7	1 MGE_CHICK	P13854 gallus gall
19	93.5	8.5	1 EKI1_YEAST	O03764 saccharomyc
20	92.5	8.4	1 YAF1_YEAST	P77339 escherichia
21	91.5	8.3	1 GCR_ONCMY	O02224 homo sapien
22	84.5	7.7	1 EGM_HUMAN	O13201 homo sapien
23	83.5	7.6	1 GCR_PAROL	O73673 paratuberculo
24	83	7.6	1 SMC2_YEAST	P38989 saccharomyc
25	82.5	7.5	1 AAC4_RAT	O09490 rattus norv
26	82	7.5	1 HS78_SCHPO	O59838 schistosach
27	82	7.5	1 GCR_ONCMY	P45834 oncorhynch
28	81.5	7.4	1 YIE1_YEAST	P40531 saccharomyc
29	81	7.4	1 IL7_BOVIN	P26895 bos taurus
30	81	7.4	1 KIME_YEAST	P07277 saccharomyc
31	81	7.4	1 KIF2_XENLA	O91637 xenopus lae
32	81	7.4	1 Y08_METJA	O60307 methanococc
33	80.5	7.3	1 Y328_MYCGE	O49419 mycoplasma

34	80.5	7.3	1111	1	KIP1_YEAST	P28742 saccharomyc
35	80	7.3	377	1	TDP_DROME	O24318 drosophila
36	80	7.3	525	1	ASF2_YEAST	P32448 saccharomyc
37	80	7.3	584	1	CNA1_DROME	P12252 drosophila
38	80	7.3	623	1	RPOC_G0ITH	O78484 guillardi
39	80	7.3	954	1	DRP2_HUMAN	O13474 homo sapien
40	79.5	7.2	555	1	VNS2_YEAST	P53877 saccharomyc
41	79	7.2	176	1	IL7_SHEEP	O28540 ovis aries
42	79	7.2	1038	1	DPD_CANAL	P46588 candida alb
43	78.5	7.1	425	1	YBQ_YEAST	P38272 saccharomyc
44	78.5	7.1	454	1	DNAI_HAEIN	P43742 haemophilus
45	78.5	7.1	515	1	TRPE_BUCAP	P42387 buchemera ep

ALIGNMENTS

RESULT	ID	IL6_MOUSE	STANDARD	PRT	211 AA.
AC	P08505:				
DT	01-AUG-1988	(Rel. 08, Created)			
DT	01-AUG-1988	(Rel. 08, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (INTERLEUKIN HP-1) (B-CELL HYBRIDOMA GROWTH FACTOR).				
DE	IL6 OR IL-6				
GN	IL6				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RM	[1]				
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.				
RX	MEDLINE=88166883; Pubmed=2965020;				
RA	van Soick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,				
RA	Boon T., Simpson R.J.;				
RT	*cDNA cloning of murine Interleukin-HP1: homology with human				
RT	Interleukin 6.*;				
RL	Eur. J. Immunol. 18:193-197(1988).				
RM	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89035525; Pubmed=3263439;				
RA	Tanabe O., Akira S., Kamaya T., Wong G.-G., Hirano T., Kishimoto T.;				
RT	*Genomic structure of the murine IL-6 gene. High degree conservation				
RT	of potential regulatory sequences between mouse and human.*;				
RL	J. Immunol. 141:3875-3881(1988).				
RM	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/C;				
RX	MEDLINE=91057159; Pubmed=2243807;				
RA	Greene H.E., Fuentes N.L., Fuller G.M.;				
RT	*Cloning and sequence analysis of the cDNA for murine Interleukin-6.*;				
RL	Nucleic Acids Res. 18:6455-6455(1990).				
RM	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89017145; Pubmed=3262872;				
RA	Chiu C.-P., Moulds C., Coffman R.L., Rennick D., Lee F.;				
RT	*Multiple biological activities are expressed by a mouse Interleukin				
RT	6 cDNA clone isolated from bone marrow stromal cells.*;				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).				
RM	[5]				
RP	SEQUENCE OF 5-211 FROM N.A.				
RC	STRAIN-C57BL/6J;				
RX	MEDLINE=89124383; Pubmed=2563387;				
RA	Mock B.A., Nordan R.P., Justice M.J., Kozak C., Jenkins N.A.,				
RA	Copeland N.G., Clark S.C., Wong G.-G., Rudikoff S.;				
RT	*The murine IL-6 gene maps to the proximal region of chromosome 5.*;				
RL	J. Immunol. 142:1372-1376(1989).				
RM	[6]				
RP	SEQUENCE OF 1-6 FROM N.A.				
RC	STRAIN-BALB/C;				
RX	MEDLINE=90171860; Pubmed=2106569;				
RA	Blankenstein T., Qin Z., Li W., Diamantstein T.;				

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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 17:36:04 ; Search time 38.09 Seconds
(without alignments)
3041.701 Million cell updates/sec

Title: US-09-230-048-1
Perfect score: 612
Sequence: 1 ATGTGCTGCTTCAAGTTTGTG.....CCTCGACGCTCCACGATTAAG 612

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:
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6: /cgn2_6/ptodata/2/ina/Backfile1.seq.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	612	100.0	615	2	US-08-748-640-1
2	612	100.0	615	2	US-08-686-349-1
3	612	100.0	35100	4	US-08-770-379-17
4	612	100.0	35100	4	US-08-757-669A-17
5	61	10.0	555	2	US-08-945-529-7
6	54.6	8.9	555	2	US-08-567-047-1
7	54.6	8.9	555	2	US-08-693-162-1
8	54.6	8.9	555	2	US-08-567-048-1
9	54.6	8.9	555	2	US-09-008-482-1
10	53.6	8.8	564	1	US-07-918-181A-3
11	53.6	8.8	564	1	US-07-918-181A-7
12	53.6	8.8	564	1	US-08-231-575-3
13	53.6	8.8	564	1	US-08-231-575-7
14	53.6	8.8	564	5	PCR-US93-06928-3
15	53.6	8.8	564	5	PCR-US93-06928-7
16	53	8.7	525	1	US-08-009-973-2
17	53	8.7	525	2	US-08-945-529-1
18	53	8.7	525	2	US-08-945-529-4
19	53	8.7	525	2	US-08-945-529-5
20	53	8.7	525	2	US-08-945-529-6
21	53	8.7	561	1	US-07-745-382-19
22	53	8.7	561	1	US-07-921-848-19
23	53	8.7	561	1	US-08-165-301A-19
24	53	8.7	561	3	US-08-810-436-19
25	53	8.7	561	3	PCR-US94-14179-19
26	52	8.5	564	1	US-07-918-181A-1
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28	52	8.5	564	1	US-08-231-575-1	Sequence 1, Appl1
29	52	8.5	564	1	US-08-231-575-5	Sequence 5, Appl1
30	52	8.5	564	5	PCR-US93-06928-1	Sequence 1, Appl1
31	52	8.5	564	5	PCR-US93-06928-5	Sequence 5, Appl1
32	51.4	8.4	540	4	US-08-149-101A-3	Sequence 3, Appl1
33	51.4	8.4	540	5	PCR-US94-12873-3	Sequence 3, Appl1
34	51.4	8.4	555	1	US-08-437-680A-1	Sequence 1, Appl1
35	51.4	8.4	561	3	US-08-469-318-175	Sequence 175, App
36	51.4	8.4	561	3	US-08-468-609A-175	Sequence 175, App
37	51.4	8.4	561	5	PCR-US95-01185-175	Sequence 175, App
38	51.4	8.4	951	3	US-08-469-318-57	Sequence 57, Appl
39	51.4	8.4	951	3	US-08-468-609A-57	Sequence 57, Appl
40	51.4	8.4	951	5	PCR-US95-01185-57	Sequence 57, Appl
41	51.4	8.4	1128	4	US-08-795-473B-1	Sequence 1, Appl1
42	51.4	8.4	1145	6	5510472-1	Patent No. 5510472
43	49.6	8.1	564	5	PCR-US92-05612-1	Sequence 1, Appl1
44	49.6	8.1	564	5	PCR-US94-04208-6	Sequence 6, Appl1
45	49.6	8.1	566	1	US-08-209-182C-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-748-640-1
Sequence 1, Application US/08748640
Patent No. 5834398
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: KAPOSI'S SARCOMA-ASSOCIATED HERPES VIRUS
TITLE OF INVENTION:
NUMBER OF INVENTION: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,640
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 51731-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..615
US-08-748-640-1


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Db 601 GTCCAGCATAG 612
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RESULT 3
US-08-770-379-17/c
; Sequence 17, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-17

Query Match 100.0%; Score 612; DB 2; Length 35100;
Best Local Similarity 100.0%; Pred. No. 2.5e-200;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 421 AATAAGCTGACTAAGACGACACTACAGTCCACCCAAATTTGACCGGGCTATTAGGAGG 480
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RESULT 4
US-08-757-669A-17/c
; Sequence 17, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757.669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-17

Query Match 100.0%; Score 612; DB 4; Length 35100;
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host local Similarity 100.0%; Pred No. 2,5e-200;
Matches 6112; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

OY 1 ATGTGCTGCTCAATGTGTGGTCTCTCTGCTGGTTCACTGCTGTAATCTGGAACG 60
    |||||
Db 17875 ATGTGCTGCTCAATGTGTGGTCTCTCTGCTGGTTCACTGCTGTAATCTGGAACG 17816

OY 61 CCGGCGCAAGTTCGCCGAGCCGCCCGAGTTTGAAAAGATCTTCATATTCAGAGACTCAAT 120
    |||||
Db 17815 CCGGCGCAAGTTCGCCGAGCCGCCCGAGTTTGAAAAGATCTTCATATTCAGAGACTCAAT 17756

OY 121 TGGATGCTATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
    |||||
Db 17755 TGGATGCTATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 17696

OY 181 AAGGTAATCTAGAACCCCGCTGTAATTTTTCATCTGAACACTACGAGCCATCAAGACTACT 240
    |||||
Db 17695 AAGGTAATCTAGAACCCCGCTGTAATTTTTCATCTGAACACTACGAGCCATCAAGACTACT 17636

OY 241 GATCACTGCGGGTTAATAGATTTTAATGAGACTAGCTGCTTAAAGCTGCGGATGCG 300
    |||||
Db 17635 GATCACTGCGGGTTAATAGATTTTAATGAGACTAGCTGCTTAAAGCTGCGGATGCG 17576

OY 301 TTTTATTTGAATTCGAGCTGTTGTTTAACTTTTAAACGACGGAAGTTTGAAATCACTGATA 360
    |||||
Db 17575 TTTTATTTGAATTCGAGCTGTTGTTTAACTTTTAAACGACGGAAGTTTGAAATCACTGATA 17516

OY 361 AAGGTGAGACTGATGAGACTCTGAGCAAGACCTTGAGATGGGAGATCAAGAGAGACTG 420
    |||||
Db 17515 AAGGTGAGACTGATGAGACTCTGAGCAAGACCTTGAGATGGGAGATCAAGAGAGACTG 17456

OY 421 AATTAAGCTACTAAGACGCACTACAGATCCACCCAAATTTGACCGGGGCTATTTAGGGAGG 480
    |||||
Db 17455 AATTAAGCTACTAAGACGCACTACAGATCCACCCAAATTTGACCGGGGCTATTTAGGGAGG 17396

OY 481 CTTTCAGGAGCTTAAGTATTTGGTGAGACACTTTTGCTTTATGTTCTGAGTGAATG 540
    |||||
Db 17395 CTTTCAGGAGCTTAAGTATTTGGTGAGACACTTTTGCTTTATGTTCTGAGTGAATG 17336

OY 541 GAAAGTTTGACAGTGCAAGCGGTCGTGTTTGGACTATATCCAGAGCTGACTCTGAC 600
    |||||
Db 17335 GAAAGTTTGACAGTGCAAGCGGTCGTGTTTGGACTATATCCAGAGCTGACTCTGAC 17276

OY 601 GTTCACGATTAAG 612
    |||||
Db 17275 GTTCACGATTAAG 17264

RESULT 5
US-08-945-529-7
: Sequence 7, Application US/08945529
: Patent No. 5972902
: GENERAL INFORMATION:
: APPLICANT: CILIBERTO, Gennaro
: APPLICANT: SAVINO, Rocco
: APPLICANT: PAONESSA, Rocco
: TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
: TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
: STREET: 419 Seventh Street N.W., Suite 300
: City: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/08/945,529
2 FILING DATE: 28-OCT-1997
3 CLASSIFICATION: 514
4 PRIOR APPLICATION DATA: IT RM95A000273
5 APPLICATION NUMBER: 28-APR-1995
6 FILING DATE: 28-APR-1995
7 PRIOR APPLICATION DATA: PCW/1796/00084
8 APPLICATION NUMBER: 26-APR-1996
9 FILING DATE: 26-APR-1996
10 ATTORNEY/AGENT INFORMATION:
11 NAME: YUN, Allen C
12 REGISTRATION NUMBER: 37,971
13 REFERENCE/DOCKET NUMBER: CILIBERTO-3
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 202-628-5197
16 TELEFAX: 202-737-3528
17 INFORMATION FOR SEQ ID NO: 7:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 555 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: double
22 TOPOLOGY: linear
23 MOLECULE TYPE: cDNA
24 US-08-945-529-7
25
26 Query Match 10.0% Score 61: DB 2: Length 555:
27 Best Local Similarity 47.3% Pred. No. 2.3e-11:
28 Matches 184: Conservative 0: Mismatches 205: Indels 0: Gaps 0
29
30 150 TGTACCCTACCGCATCTGCAAGGGTATTCTAGAGCCGCTGCTATTTCATCTGAA 219
31      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
32 Db 130 TGTAAACAAGTATCATGTGTGAACACAGCAAGAGCGCGCATTTCTGGAACTGANC 189
33      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 Oy 220 CTACACGACATCAACGATTAATGATCACTGGGGTAAATAGATTAAGAGACTGAC 279
35      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 Db 190 CTTCCAAAGATGGCTGTGAAAAAGACGATGCTTCTACAAAGATTCAATAGAGAGACTTGC 249
37      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
38 Oy 280 CTTAAAGCTGCGCGATGCTTTTGAATTCGAGGTGTTGTTAACTTTTAAACGACG 339
39      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 Db 230 CTGTGTGAAATCAATCACTGTGCTTTTCGATTTGAGATTACCTGATACCTCCGAMC 309
41      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
42 Oy 340 GAGTTTGGAAAAATCAGTGATAAAGCGAGCATGAGCTTCTACAGAACGACTTAGA 399
43      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
44 Db 310 AGATTTGAGATAGTAGAGAACAGCAGAGCTGTCAGATGCGACAAAAGACTGATC 369
45      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
46 Oy 400 TGGGACATACAGGAAGCTCATTAAGCTGACTAAGAGCCACTAAGTCCACCCAAATT 459
47      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 Db 370 CAGTTCCTCGGAAAAAGCCAAAGATCTAGATGCAATTAACCACTGAGCCCAACACA 429
49      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
50 Oy 460 GACCGCGATCTATTAGGAGGCTTCAGGAGCTTAAGTATTGGTGGAGACCTTGTG 519
51      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 Db 430 AATGCCAGCTGCTGACGAGCTGACGACAGCAAGAACCAAGTGGCTGACGACATGCANCT 489
53      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
54 Oy 520 TTTTATGTCGAGTGCATGCAATGCAAAAGTT 548
55      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
56 Db 490 CATCTCATTCGCGCAGCTTTAAGGAGTT 518
57      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
58
59 RESULT 6
60 US-08-567-047-1
61 ; Sequence 1, Application US/08567047
62 ; Patent No. 5789552
63 ; Patent No. 5789552 5789555
64 ; GENERAL INFORMATION:
65 ; APPLICANT: SAVINO, ROCCO
66 ; APPLICANT: LAHM, Armin
67 ; APPLICANT: CILIBERTO, Gennaro
68 ; TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
69 ; TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
70 ; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
71 ; NUMBER OF SEQUENCES: 15
72 ; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,047
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no
FRAGMENT TYPE: Internal
IMMEDIATE SOURCE:
LIBRARY: production in bacteria
FEATURE:
NAME/KEY: IL-6 cDNA
IDENTIFICATION METHOD: polyacrylamide gel
FEATURE:
NAME/KEY: CDS
LOCATION: 1..552
US-08-567-047-1

Query Match 8.9%; Score 54.6; DB 1; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 160 TGTACCGTACCGGATCTGCAAGGGTATTTAGAGCCCGCTGCTATTTTTCATCTGAAA 219
DB 130 TGTAAACAAGTAACTGTGTGAACACCAAGAGGCACTGCGCAAGAAAACAACTGAAC 189
QY 220 CTACGACGATCAACATCTGATCCTGCGGGTTAATAGATTAAATGAGACTAGTGC 279
DB 190 CTTCGAAAGATGCTGAAAAAAGATGATCTTCCAAATCTGGATTCAATGAGAGAACTTG 249
QY 280 CTTTAAAGCTGCCCATGCTTTTGAATTGCGAGCGTGTGTTTAACTTTTAAACAGC 339
DB 250 CTGCTGAAATTCATCACTGCTCTTTGGAGTTGAGTATACCTAGATACCTCCAGAAC 309
QY 340 GAGTTGGAATAACAGTATTAACGTGACGTCATGAGCTTTCAGCAAGACCTTAGA 399
DB 310 AGATTGAGAGTGTGAGGAGCAAGCCAGAGCTGTCCAGATGATGATGACAAAGTCTGATC 369
QY 400 TGGACATTAAGAGAGCTCAATAGCTGACTAAGACGCACTACAGTCCACCAAAATTT 459
DB 370 CAGTCTCTGAGAAAAAGGCAATCTAGATGCAATTAACACCCCTGACCAACACACA 429
QY 460 GACCGCGCTATTAGGAGAGCTTCAGGAGCTTAAGTATTTGGTGAGACACTTCTTCG 519

DB 430 AATGCCAGCTGCTGACGAAGCTGCAGGACAGACCAAGTGGCTGACAGCATGACACT 489
QY 520 TTTTANGTCTGAGTGCATGGAAGATT 548
DB 490 CATCTCATCTCGAATCTTTTAAAGAGATT 518

RESULT 7
US-08-693-182-1
Sequence 1, Application US/08693182
Patent No. 5849283
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHN, Armin
APPLICANT: TONIAZZI, Carlo
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
TITLE OF INVENTION: MODELLING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Newmark, P. L. L. C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A000805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CILIBERTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..552
US-08-693-182-1

Query Match 8.9%; Score 54.6; DB 2; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 160 TGTACCGTACCGGATCTGCAAGGGTATTTAGAGCCCGCTGCTATTTTTCATCTGAAA 219
DB 130 TGTAAACAAGTAACTGTGTGAACACCAAGAGGCACTGCGCAAGAAAACAACTGAAC 189
QY 220 CTACGACGATCAACATCTGATCCTGCGGGTTAATAGATTAAATGAGACTAGTGC 279

Db 190 CTTCCAAAGATCGCTGCAAAAGATGATGCTTCCAACTCTGCAATTCGATTAATGAGAGCACTTGC 249
QY 280 CTTAAAGAGCTGCGCGATGCGCTTTTGAATTCGAGGTGTGTTTAACTTTTAAAGCAGC 339
Db 250 CTGGTGAAGAAATCATACGTCGCTTTTGAAGTTTGAAGTAACTTAACCTTAAGACCTCCAGAAC 309
QY 340 GAGTTTGGAAATCATGATTAACCTGAGCTCATGAGCTTCTGACGAAGACCTTAGA 399
Db 310 AGATTGTGAGTAGTAGAGATGCAAGCAGAGCTGTCCAGATGATGCAAAAGTCCGATC 369
QY 400 TGGGACATACAGAGACCTCAATTAACCTGACTTAAGCAGCAGCTACAGTCCACCAATTT 459
Db 370 CAGTTCCTGCGCAAAAGCAAGAAATCTAGATGCAATTAACCAACCCCTGACCAACACACA 429
QY 460 GACCGCGCTATTAAGGAGGCTTCAGGACTTAAGTATTTGGTGAGACACTTGTCTGC 519
Db 430 AATGCCACCTCTGACCAAGCTGACGACAGACAGACAGTGGCTGACAGACATGACAACT 489
QY 520 TTTTATCTTCGAGTCAATGGAAGTT 548
Db 490 CATCTCATCTGAGATCTTTTAAGAGTT 518

RESULT 8
US-08-567-048-1
Sequence 1, Application US/08567048
Patent No. 5891998

GENERAL INFORMATION:

APPLICANT: SAVINO, ROCCO
APPLICANT: LAHM, Armin
TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,048
CLASSIFICATION: 530
FILING DATE: 04-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no

FRAGMENT TYPE: Internal
IMMEDIATE SOURCE:
LIBRARY: production in bacteria
FEATURE:
NAME/KEY: IL-6 cDNA
IDENTIFICATION METHOD: polyacrylamide gel
FEATURE:
NAME/KEY: CDS
LOCATION: 1..552
US-08-567-048-1

Query Match 8.9%, Score 54.6; DB 2; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 160 TTTTACCGTACCGGATCTGCAAGGCTTCTTCAAGCCCGCTCTATTTCATCTGAAA 219
Db 130 TGTAAAGAGTAAATCTGTGAAAAGCAAGAGGCAAGGCACTGGCAGAAAACCACTGAAC 189
QY 220 CTACCAAGCATCAAGATACATGATCGCGGTTAATAGATTTAATGAGTACGTCG 279
Db 190 CTTCCAAAGATGGCTGAAAAGAAAGATGATGCTTCCAACTGTGATCAATGAGGAGACTTGC 249
QY 280 CTTAAAGAGCTGCGCGATGCTTTTGAATTCAGAGGCTGTGTTAAGTTTAAAGCAGC 339
Db 250 CTGGTGAAGATCATCATCGTCTTTTGGAGTTTGGAGTTACCTAGACCTCCAGAAC 309
QY 340 GAGTTTGGAAATCATGATTAACCTGAGCTCATGAGCTTCTGACGAAGACTTAGA 399
Db 310 AGATTGTGAGTAGTAGAGCAAGCCAGAGCTGTCCAGATGATGACAAAGTCCGATC 369
QY 400 TGGACATACAGGAAGACCTCAATTAAGCTGACTAAGCAGCACTACAGTCCCAATTT 459
Db 370 CAGTTCCTGCAAAAAGCAAGAAATCTAGATCAATTAACCAACCCCTGACCAACACA 429
QY 460 GACCGCGCTATTAAGGAGGCTTCAGGACTTAAGTATTTGGTGAGACACTTGTCTGC 519
Db 430 AATGCCACCTCTGACAGAGCTGAGGACAGAACCAAGTGGCTGAGAGACATGACAACT 489
QY 520 TTTTATCTTCGAGTCAATGGAAGTT 548
Db 490 CATCTCATCTGAGATCTTTTAAGAGTT 518

RESULT 9

US-09-008-482-1
Sequence 1, Application US/09008482

Patent No. 5914106

GENERAL INFORMATION:

APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, ROCCO
APPLICANT: LAHM, Armin
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPERANTAGONISTS OF HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,482


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: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/693,182
: FILING DATE: 14-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IT95/00216
: FILING DATE: 13-DEC-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IT RM 94A000805
: FILING DATE: 14-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: YUN, Allen C.
: REGISTRATION NUMBER: 37,971
: REFERENCE/DOCKET NUMBER: CILIBERTO-2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ. ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 555 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..552
: US-09-008-482-1

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Query Match      8.9%; Score 54.6; DB 2; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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QY 160 TGTACCGTCACCGCATCTGCAAGGATATTCTAGAGCCCGCTGATTTTCATCTGAAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 TGTACCAAGTACATGTTGTGAACACGACAAAGAGCGCTGCGAGAAAACACCTGAC 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 220 CTACACCCATCAACGATACGATCAGTCGCGGTTAATAGATTAAAGACTAGACTGTC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 CTTCCAAGATGCGCTGAAGAAAGATGATGCTTCCATCTGATTCAGAGAGACTGTC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 280 CTTAAAGAGCTCCGCGATGCTTTTGAATTCAGAGTCTTTTAAAGTTTAAAGCAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 CTGCTGAAATACATCACTGCTGCTTTGAGTTGAGTAAACCTGATACCTCCAGAAC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 340 GAGTTTGAATAATCACTGATTAACGTCGACGTCATGAGCTTCTGACGAGACCTTAAGA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 310 AGATTTGAGTAGTAGAGTCAAGCAGAGCTGTCAGATGATGATCAAAAGTCTGATC 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 TGGACATACAGGAAGAGCTCAATAGCTGACTAAGACCACTACAGTCCACCAATTT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 370 CAGTTCCTGCGAAGAAAGCAAAATCTAGATGCAATACCACTGACCCAGCCACACA 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 GACCGCGCTATTAGGAGGCTTCAGGACTTAAGTATTGGTAGACACTTTCCTTCG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 430 AATGCCAGGCTGCTGAGCAAGAGCTGACAGGCAAGAACCACTGCTGACAGACATGACACT 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 TTTATGTTCTGATGCAATGCAAAACTT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 490 CATCTCATCTGAGATCTTTTAAGAGATT 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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```

RESULT 10
US-07-918-181A-3
: Sequence 3, Application US/07918181A
: Patent No. 5338833
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Muteins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated

```

```

: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/918,181A
: FILING DATE: 23-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: FOW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ. ID NO. 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 564 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..558
: FEATURE:
: NAME/KEY: met_peptide
: LOCATION: 1..555
: US-07-918-181A-3

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Query Match      8.8%; Score 53.6; DB 1; Length 564;
Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

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QY 154 GACCTGTACCGTCACCGCATCTGCAAGGATATTCTAGAGCCCGCTGCTATTTTTCAT 213
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DB 127 GAGACCTCTTAACAAGAGTACATGTGTGAAGCAGTAAAGACACTGGCAGAAAAACAC 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 214 CTGAACCTACAGCAGATCAAGATGATCACTGCGGGTTAATGAGATTAAAGAGACT 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 CTGAACCTTCCGAAGATGCGCTGCAAAAAAGATGATGTTTCAATCTGATTCATAGCAA 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 ACGTCCCTTAAAGAGCTGCGCGATGCTTTTGAATTCGAGGTGTTGTTAAGTTTAA 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 247 ACTGTCTGTGGAATAATCATCAAGCGCTTTTGAATTTGAGTATACCTAAGTACCTC 306
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QY 334 ACGAGGAGTTTGAATAATCATGATTAACGTGAGCTCATGAGAGCTTTCAGCAAGAGC 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 CAGAACATATTGAGATGAGTAGAGGAACCAAGCAGAGCTGTCCAGATTCGACCAAAAGTC 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 TTAGATGGACATPACAGGAAGAGCTCAATAGCTGATGAGAGCACTACAGTCCACC 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 367 CTGATCCAGATTCTGCGAAGAAAGCAAAAAAATCTGATGCAATAAACCCCGGATCCA 426
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QY 454 AAATTGACCCCGCTATTAGGAGGCTTCAGGAGACTTAAGTATTGGTGGAGACACTTT 513
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DB 427 ACCAAMATGAGAGCTGTGAGCAAGCTGCAAGCAGACAGACAGAGTGGTGCAGGACATG 486
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QY 514 GCTTGCTTTATGTTGAGTGCATGAGAAAGTTTCAGAGTCAAGCGGTGCTGCTTTTG 573
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DB 487 ACAACTCATTCATCTGAGATCTTTGAAAGAAATCTCCAGATCCCTCCCTGCTGCTG 546
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RESULT 11

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US-07-918-181A-7
: Sequence 7, Application US/07918181A
: Patent No. 5338833
: GENERAL INFORMATION:
: APPLICANT: Fowles, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varlick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/918,181A
: FILING DATE: 23-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheels, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: POW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 564 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: AMTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..558
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 1..555
: US-07-918-181A-7

Query Match      8.8%: Score 53.6; DB 1; Length 564;
Best Local Similarity 45.5%: Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 154 GACCTCTGTTACCGTACCGGCAATGCAAGGCTATTCTAGAGCCCGCTGCTATTTCAT 213
DB 127 GAGAGCTGTAAACAGATGATGTGTAAAGCAAGTAAAGACACTGGCAGAAACAC 186
QY 214 CTGAACCTACGACCATCAACCATACATGATCAGCGGTTAAATAGATTAAATGAGACT 273
DB 187 CTGAACCTTCGACAGATGCGTGAATAAAGATGATGTTTCAATCTGATCAATGAGAA 246
QY 274 AGCTGCTTAAAGCTGCGGATGCTTTTGAATTCGAGGTGTTAGATTATTTTA 333
DB 247 ACTTGTCTGCTGAATATCAATCAAGCGCTTTTGAATTTGATATACCTAGAGTACCTC 306
QY 334 ACAGAGCACTTTGCAAAATCACTGATTAACCTGACCTCATGACCTTCTGACGAAGACC 393
DB 307 CAGAACAGATTTGAGAGTAGTAGAGCAACGAGAGCTGTCCAGATGTCCAGCAAAAGTC 366
QY 394 TTAGATGCGACATACAGCAAGACGCTCAATTAACCTGACTAAGACGCACTACACTCCACC 453
DB 367 CTGATGCACTTTCTCCAGAAAGGCAAAATCTAGATGCAATTAACCAACCCGGATCCA 426
QY 454 AATTTTGAACGCGGCTCTATTAGGAGGCTTCAGGAGCTTAAGTATTGGGTGAGACACTTT 513

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DB 427 ACACAAATGCGAGCTGCTGACGAGAGCTGACAGACAGAAACAGTGGCTGACAGACATG 486
QY 514 GCTTCGTTTATGCTGTGAGTGCATGCAATGCAAAAGTTTGACGCTCAAGCGTCCGTGTTTG 573
DB 487 ACAACTCATCTCATCTGTGAGATCTTGAAGAATTCATGACAGTCCCTCCGCTGCTCG 546

RESULT 12
US-08-231-575-3
: Sequence 3, Application US/08231575
: Patent No. 5565336
: GENERAL INFORMATION:
: APPLICANT: Fowles, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varlick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/231,575
: FILING DATE: 22-APR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/918,181
: FILING DATE: 23-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheels, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: POW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 564 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: AMTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..558
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 1..555
: US-08-231-575-3

Query Match      8.8%: Score 53.6; DB 1; Length 564;
Best Local Similarity 45.5%: Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 154 GACCTCTGTTACCGTACCGGCAATGCAAGGCTATTCTAGAGCCCGCTGCTATTTCAT 213
DB 127 GAGAGCTGTAAACAGATGATGTGTAAAGCAAGTAAAGACACTGGCAGAAACAC 186
QY 214 CTGAACCTACGACCATCAACCATACATGATCAGCGGTTAAATAGATTAAATGAGACT 273
DB 187 CTGAACCTTCGACAGATGCGTGAATAAAGATGATGTTTCAATCTGATCAATGAGAA 246
QY 274 AGCTGCTTAAAGCTGCGGATGCTTTTGAATTCGAGGTGTTAGATTATTTTA 333

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Db 247 ACTGTCTGGTGAATAATCATCATCAGAGCCTTTGGAAATTTGAGGTACTACTACTACT 306
QY 334 ACACAGGAGTTTGGAAATCAGTGAATAAACGTGCACGTCAATGAGCTTCTACCAAGACC 393
Db 307 CAGAACGATTGTAGAGTAGTGAAGAACGAGAGCTGTCCATATCTGCACCAAGATC 366
QY 394 TTAGATGAGCATATACGAGAGAGCTCAATAGCTAGCTAGAGACCACTACAGTCCACC 453
Db 367 CTGATCCAGTTTCTGCAGAAAAGGCAAAATCTAGATCCATATACACCCCGCATCCA 426
QY 454 AAATTGACCGCGCTCTATTAGGAGCTTCAGGACTTAACTATTGGGTAGACACTTT 513
Db 427 ACCAATAATCGAGCCTGTCTGACAGCTGCAGGACAGAACCACTGCTCAGGACATG 486
QY 514 GCTTCGTTTATGTTCTGAGCTGCAATGAAAAGTTTGCAGTCAAGCGGCTGTTTGT 573
Db 487 ACAACTCATCTCATCTTGAGATCTTTGAAAGAAATTCCTGCAATCTCTCCCTGCTG 546

RESULT 13
US-08-231-575-7
Sequence 7, Application US/08231575
Patent No. 5565336

GENERAL INFORMATION:

APPLICANT: Fowles, Dana M.

TITLE OF INVENTION: C-Terminal IL-6 Mutelins

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/231,575

FILING DATE: 22-Apr-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/918,181

FILING DATE: 23-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Sheets, Eric J.

REGISTRATION NUMBER: 30,326

REFERENCE/DOCKET NUMBER: FOW-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405

TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 564 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..558

FEATURE:

NAME/KEY: mat.peptide

LOCATION: 1..555

US-08-231-575-7

Query Match 8.8%; Score 53.6; DB 1; Length 564;

Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 154 GACCTCTGTTACCTACCGCATCTGCAGAGGATTTAGAGCCCGCTGTATTTTCAT 213
Db 127 GAGACCTGTAACCAAGATACATGTGTGAAGAGTAAAGAGCATCTGCAGAAACAC 186
QY 214 CTGAACCTACGAGCATCAAGATAGTACTGACTGCGGGTCTTAATAGATTAAGACT 273
Db 187 CTGAACCTTCGGAAGATAGCTGTAAGAAAGATGATGTTTTCATCTGATTAATAGAG 246
QY 274 AGCTGCTTAATAAGCTGCCCATGCGTTTGTGAATTCAGAGGTGTGTTAAGTTTGA 333
Db 247 ACTGTCTGGTGAATAATCATCATCAGAGCCTTTGGAAATTTGAGGTACTACTAGAC 306
QY 334 ACACAGGAGTTTGGAAATCAGTGAATAAACGTGCACGTCAATGAGCTTCTACCAAGACC 393
Db 307 CAGAACGATTGTAGAGTAGTGAAGAACGAGAGCTGTCCATATCTGCACCAAGATC 366
QY 394 TTAGATGAGCATATACGAGAGAGCTCAATAGCTAGCTAGAGACCACTACAGTCCACC 453
Db 367 CTGATCCAGTTTCTGCAGAAAAGGCAAAATCTAGATCCATATACCAACCCCGATCCA 426
QY 454 AAATTGACCGCGCTCTATTAGGAGCTTCAGGACTTAACTATTGGGTAGACACTTT 513
Db 427 ACCAATAATCGAGCCTGTCTGACAGCTGCAGGACAGAACCACTGCTCAGGACATG 486
QY 514 GCTTCGTTTATGTTCTGAGCTGCAATGAAAAGTTTGCAGTCAAGCGGCTGTTTGT 573
Db 487 ACAACTCATCTCATCTTGAGATCTTTGAAAGAAATTCCTGCAATCTCTCCCTGCTG 546

RESULT 14
PCT-US93-06928-3

Sequence 3, Application PC/TUS9306928

GENERAL INFORMATION:

APPLICANT: Fowles, Dana M.

TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 11014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06928

FILING DATE: 1993/07/23

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/918,181

FILING DATE: 23-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pelt, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: FOW-2-T

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405

TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 564 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
PCT-US93-06928-3

Query Match 8.8%; Score 53.6; DB 5; Length 564;
Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

154 GACCTGTTTACCGTCACGAGTATTCAGACCCGCTGATTTTTCAT 213
127 GAGACCTGTACAGAGTAACTGTGTGAACGACTAAAGACACCTGGAGAAACAC 186
214 CTGAACCTACACCCATCAAGATCTGATCACTGCGGGTTAATAGATTTAGACT 273
187 CTGAACCTTCCGAAAGTCCCTGAAAAAGATGATGTCTTTCATCTGATTCATAGAGAA 246
274 AGCTCCCTTAAAAAGCTCCGATGCTTTTGAATTCGAGTGTGTTTAACTTTTAA 333
247 ACTTGTGTGTGAATTCATCAGAGCCTTTTGGATTTGAGTATACCTAGAGTACTC 306
334 ACAGACGACTTTGCAAAATCAGTGAATTAACGTGACGTGATGAGCTTTCAGCAAGACC 393
307 CAGAACAGATTTTCAGAGTGTGAGCAACACGAGCTGTCCAGATGTCCAGCAAGATC 366
394 TTAGATGGACATACAGAGAGCTCAATTAAGTGAAGTACAGTACAGTCCAGCC 453
367 CTGATCCAGTTTCTGCAAGAAAGCAAAATCTAGATGCAATTAACACCCCGATCCCA 426
454 AAATTTGACCCCGCTTATTACGAGCCTTCAGGACTTAAGTATGCTGACACACTTT 513
427 ACCAACAATGCGAGCTGTGACGAAGCTGCAAGACCAACCGTGGCTGAGAGCATG 486
514 GCTTCGTTTATGTTCTGAGTCAATGCAAAAGTTTCACGCTCAACGCGTCCGCTTTTG 573
487 ACAACGATCTCATTTCTGAGATCTTTGAAGAATTCCTGCGAGTCCCTCCCTGCTCTG 546

RESULT 15
PCT-US93-06928-7
Sequence 7, Application PC/US9306928
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varlick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
NAME/KEY: mat_peptide
LOCATION: 1..555
PCT-US93-06928-7

Query Match 8.8%; Score 53.6; DB 5; Length 564;
Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

154 GACCTGTTTACCGTCACGAGTATTCAGACCCGCTGATTTTTCAT 213
127 GAGACCTGTAAAGATGATGTGTGAAGCAAGTAAAGACACCTGGAGAAACAC 186
214 CTGAACCTACACCCATCAAGATCTGATCACTGCGGGTTAATAGATTTAGACT 273
187 CTGAACCTTCCGAAAGTCCCTGAAAAAGATGATGTCTTTCATCTGATTCATAGAGAA 246
274 AGCTCCCTTAAAAAGCTCCGATGCTTTTGAATTCGAGTGTGTTTAACTTTTAA 333
247 ACTTGTGTGTGAATTCATCAGAGCCTTTTGGATTTGAGTATACCTAGAGTACTC 306
334 ACAGACGAGTTTTCAGAAATCAGTGAATTAAGTGAAGTCAATGAGCTTCGAGCAAGACC 393
307 CAGAACAGATTTTCAGAGTGTGAGCAACACGAGCTGTCCAGATGTGACCAAAAGTC 366
454 AAATTTGACCCCGCTTATTACGAGCCTTCAGGACTTAAGTATGCTGACACACTTT 513
427 ACCAACAATGCGAGCTGTGACGAAGCTGCAAGACCAACCGTGGCTGAGAGCATG 486
514 GCTTCGTTTATGTTCTGAGTCAATGCAAAAGTTTCAGAGTCAAGCGTCCGCTTTTG 573
487 ACAACGATCTCATTTCTGAGATCTTTGAAGAATTCATTCAGTCCCTCCCTGCTCTG 546

Search completed: October 4, 2001, 18:48:57
Job time: 4373 sec

Fri Oct . 5 10:02:05 2001

us-09-230-048-1.rni

Page 11

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:14 ; Search time 74.43 seconds

(without alignments)
362.626 Million cell updates/sec

Title: US-09-230-048-2

Perfect score: 1095

Sequence: 1 MCFKMLSLVGLVSLVSGT.....GQAVRLDISIPDPVHDK 204

Scoring table: BLOSUM62

Capop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MMC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_UNCLASSIFIED:*
13: SP_VIRTEBRATE:*
14: SP_VIRUS:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	14 Q98823	Q98823 Kaposi's sa
2	1093	99.8	204	14 Q40918	Q40918 Kaposi's sa
3	182	16.6	209	6 Q9TTH3	Q9TTH3 actus lemur
4	179	16.3	209	6 Q97540	Q97540 actus nancy
5	158	14.4	208	6 Q9XW80	Q9XW80 delphinapt
6	154.5	14.1	207	6 Q9MY27	Q9MY27 canis famli
7	143	13.1	175	6 Q9TTH4	Q9TTH4 actus nigril
8	138	12.6	207	11 Q9JTH3	Q9JTH3 marmota mon
9	136.5	12.5	207	6 Q28403	Q28403 enhydra lut
10	132	12.1	160	6 Q97535	Q97535 actus vocif
11	129.5	11.8	210	11 Q9WV08	Q9WV08 mesocricetu
12	116.5	10.6	241	6 Q9MZR1	Q9MZR1 oryctolagus
13	95	8.7	684	4 Q9UKF6	Q9UKF6 homo sapien
14	95	8.7	684	11 Q9GXR7	Q9GXR7 mus musculu
15	92.5	8.4	101	11 Q95041	Q95041 cricetus
16	87.5	7.9	487	1 Q28450	Q28450 archaeoglob
17	86.5	7.6	979	1 Q05477	Q05477 sulfolobus
18	83.5	7.5	145	6 Q9W205	Q9W205 oryctolagus
19	82.5	7.5	145	6 Q9W205	Q9W205 oryctolagus

20	82	7.5	367	14 Q41165	Q41165 parametium
21	81.5	7.4	442	5 Q90605	Q90605 stylyonchla
22	80.5	7.4	387	10 Q9LD24	Q9LD24 chlorarachn
23	79.5	7.3	1030	3 Q9P918	Q9P918 plicha angu
24	79	7.2	385	5 Q96442	Q96442 caenorhabdi
25	78.5	7.2	387	10 Q9ZT01	Q9ZT01 chlorarachn
26	78.5	7.2	674	5 Q95NL3	Q95NL3 chlorarachn
27	78.5	7.2	674	5 P90755	P90755 caenorhabdi
28	78	7.1	118	6 Q9M208	Q9M208 lepus callif
29	78	7.1	118	6 Q9M207	Q9M207 lepus towns
30	78	7.1	900	10 Q9FTU0	Q9FTU0 arabidopsis
31	77.5	7.1	353	14 Q65121	Q65121 african swi
32	77	7.0	486	10 Q9L169	Q9L169 arabidopsis
33	77	7.0	1004	1 Q28412	Q28412 archaeoglob
34	77	7.0	1810	10 Q9ZSD1	Q9ZSD1 lactuca sat
35	76.5	7.0	461	2 Q94647	Q94647 schizosach
36	76	6.9	1005	2 Q9HTE6	Q9HTE6 pseudomonas
37	76	6.9	1849	5 Q90487	Q90487 loligo peal
38	75.5	6.9	164	5 Q44835	Q44835 caenorhabdi
39	75.5	6.9	236	5 Q9N4D9	Q9N4D9 caenorhabdi
40	75.5	6.9	443	10 Q9LKT8	Q9LKT8 thalassios
41	75.5	6.9	448	10 Q9SMD0	Q9SMD0 zinnia eleg
42	75.5	6.9	602	2 Q9Z7J0	Q9Z7J0 chlamydia p
43	75.5	6.9	1158	3 Q9UR75	Q9UR75 schizosach
44	75	6.8	244	2 Q9W214	Q9W214 thermotoga
45	75	6.8	324	5 Q77098	Q77098 caenorhabdi

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	204 AA.
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AC	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DI	INTERLUKIN-6 HOMOLOG (FRAGMENT).			
GN	VIL-6.			
OS	Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).			
OC	viruses; dsDNA viruses; no RNA stage; Herpesviridae;			
OC	Gammapherpesvirinae; Rhadinovirus.			
OX	NCBI_TaxID=37296;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,			
RA	Friedman-Kien A.E., Fleckenstein B.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Nicholas J., Ruvoilo V.R., Burns W.H., Sandford G., Wan X., Clufo D.,			
RA	Hendrickson S., Guo H.G., Hayward G.S., Reitz M.S.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Moore P.S., Bashoff C., Weiss R.A., Chang Y.;			
RT	"Molecular mimicry of human cytokine and cytokine response pathway			
RT	genes by KSHV."			
RL	Science 274:1739-1744(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-97121480; PubMed-8962146;			
RA	Russo J.J., Bohanzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,			
RA	Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;			
RT	"Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus			
RT	(HHV8)."			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Russo J.J., Bohanzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,			
RA	Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;			

RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Petrucci D., Edelman I.S., Chang Y., Moore P.S.;
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 RM 171
 RP SEQUENCE FROM N.A.
 RA Sun R., Lin S.-F., Miller G.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U73655; AAB18244.1; -;
 DR EMBL: U67774; AAB61701.1; -;
 DR EMBL: U75698; AAC57089.1; -;
 DR EMBL: U71365; AAC34937.1; -;
 DR InterPro: IPR003573; -;
 DR Pfam: PF00489; IL6; 1.
 DR SMART: SM00126; IL6; 1.
 DR NON_TER 204
 FT SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EE CRC64;

Query Match 100.0%; Score 1095; DB 14; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.3e-99;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCMFKLSLLVSGSLVSGTRGKLPAPAFEFKDLIQRLNMLWVIDCFDLCYRTGIC 60
 DB 1 MCMFKLSLLVSGSLVSGTRGKLPAPAFEFKDLIQRLNMLWVIDCFDLCYRTGIC 60
 OY 61 KGLEPAATFHLKLPAINDDHCGLIGFNETSCLKLLADGFEFEVLFKFLTFEFGKSVI 120
 DB 61 KGLEPAATFHLKLPAINDDHCGLIGFNETSCLKLLADGFEFEVLFKFLTFEFGKSVI 120
 OY 121 NVDVWELLFTLMDIQEELINKLTKTHYSPPKFDRGLGRLQGLKYWVRHFAFVYLSAM 180
 DB 121 NVDVWELLFTLMDIQEELINKLTKTHYSPPKFDRGLGRLQGLKYWVRHFAFVYLSAM 180
 OY 181 EKFAQAVRVLDSPVTPDVYDK 204
 DB 181 EKFAQAVRVLDSPVTPDVYDK 204

RESULT 2
 ID 040918 PRELIMINARY; PRT: 204 AA.
 AC 040918:
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE ORF K2.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OC NCBI_TaxID=37296;
 RN 111
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97138401; PubMed-8985427;
 RA Neipel F., Albrecht J.C., Fleckenstein B.;
 RA Friedlan-Klen A.E., Fleckenstein B.;
 RT "Human herpesvirus 8 encodes a homolog of interleukin-6.";
 RL J. Virol. 71:839-842(1997).
 RM 121
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97296220; PubMed-9151804;
 RA Neipel F., Albrecht J.C., Fleckenstein B.;
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
 human herpesvirus 8: determinants of its pathogenicity?";
 RL J. Virol. 71:4187-4192(1997).
 DR EMBL: U93872; AAB62676.1; -;
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR Pfam: PF00489; IL6; 1.
 DR ProDom: PD004356; -; 1.

DR SMART: SM00126; IL6; 1.
 SO SEQUENCE 204 AA; 23408 MW; 2F46737828AF20B9 CRC64;

Query Match 99.8%; Score 1093; DB 14; Length 204;
 Best Local Similarity 99.5%; Pred. No. 2e-99;
 Matches 203; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCMFKLSLLVSGSLVSGTRGKLPAPAFEFKDLIQRLNMLWVIDCFDLCYRTGIC 60
 DB 1 MCMFKLSLLVSGSLVSGTRGKLPAPAFEFKDLIQRLNMLWVIDCFDLCYRTGIC 60
 OY 61 KGLEPAATFHLKLPAINDDHCGLIGFNETSCLKLLADGFEFEVLFKFLTFEFGKSVI 120
 DB 61 KGLEPAATFHLKLPAINDDHCGLIGFNETSCLKLLADGFEFEVLFKFLTFEFGKSVI 120
 OY 121 NVDVWELLFTLMDIQEELINKLTKTHYSPPKFDRGLGRLQGLKYWVRHFAFVYLSAM 180
 DB 121 NVDVWELLFTLMDIQEELINKLTKTHYSPPKFDRGLGRLQGLKYWVRHFAFVYLSAM 180
 OY 181 EKFAQAVRVLDSPVTPDVYDK 204
 DB 181 EKFAQAVRVLDSPVTPDVYDK 204

RESULT 3
 ID 09TH3 PRELIMINARY; PRT: 209 AA.
 AC 09TH3:
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus lemurinus (Northern gray-necked night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=43147;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
 RA Palatroyo M.E.;
 RT "Aotus lemurinus gene for IL-6.";
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF097323; AAF21298.1; -;
 DR HSSP: P05231; IAU.
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFPGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6; 1.
 DR SMART: SM00126; IL6; 1.
 DR NON_TER 1
 FT NON_TER 209
 FT SEQUENCE 209 AA; 23115 MW; AOA3DFAABF560CC CRC64;

Query Match 16.6%; Score 182; DB 6; Length 209;
 Best Local Similarity 26.5%; Pred. No. 4.5e-10;
 Matches 41; Conservative 36; Mismatches 78; Indels 0; Gaps 0;

OY 37 ORLMMMLWVIDCFDLCYRTGICGLLEPAATFHLKLPAINDDHCGLIGFNETSCLK 96
 DB 55 KHRIYLEGISALRKEICDSKNCSSKALLENMLPKNAEKDCQSGFNETCLVK 114
 OY 97 LADFFFEVLFKFLTFEFGKSVINVDVWELLFTLMDIQEELINKLTKTHYSPPKFDRG 156
 DB 115 IITGLFEVYLEYLRNRFESSKEQAGAVQMKSTGLISLQKKAENLSAITPDPAVNAS 174
 OY 157 LIGRLQGLKYWVRHFAFVYLSAMEKFAQAVRV 191
 DB 175 LIAKIQADQWVLDGVTHILIRSKFEFLQSSIRAL 209

[illegible][illegible]

Db 127 NEEGDEKENVKSVHSTKTLVGMKLSKKRQNDVEVTPDPPTDASLQAILQSDDEMLKHTTI 186

RESULT	7
ID	09TH14
AC	09TH14
AC	PRELIMINARY:
AC	PRT: 175 AA.
DT	01-MAY-2000 (TREMblrel. 13, Created)
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE	INTERLEUKIN-6 (FRAGMENT).
DE	IL-6.
OS	Actus nigricens (black-headed night monkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus
OX	NCBI_TaxID=57175;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA	Acturayo M.E.;
RT	"Actus nigricens gene for IL-6.";
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AF097332; AF21297.1; -
DR	HSP: P05231; IAUU
DR	InterPro: IPR002059; -
DR	InterPro: IPR003573; -
DR	InterPro: IPR003574; -
DR	Pfam: PF00489; IL6; 1.
DR	PRINTS: PR00433; IL6GSPMGF.
DR	PRINTS: PR00434; INTERLEUKIN6.
DR	ProDom: PD002435; ?; 1.
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.
DR	SMART: SM00126; IL6; 1.
FT	NON_TER
FT	SEQUENCE 175 AA: 19205 MW: 28CCE574CDB9B189 CRC64;

RT	RT	The Woodchuck interleukin-6 Gene : Cloning and Structural Analysis.	
RL	Submitted (JUL-1997)	to the EMBL/Genbank/DBJ databases.	
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	LI D.H., Cullen J.M.;		
RT	"Gene Structure of the woodchuck interleukin-6.";		
RL	Submitted (JAN-1999)	to the EMBL/Genbank/DBJ databases.	
DR	EMBL; AF012908; AAC34851.1; -		
DR	EMBL; AF122896; AAC28873.1; -		
DR	InterPro; IPR003573; -		
DR	InterPro; IPR003574; -		
DR	Pfam; PF00489; IL6; 1.		
DR	PRINTS; PRO0433; IL6CSFNGF.		
DR	PRINTS; PRO0434; INTERLEUKIN6.		
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.		
DR	SMART; SM00126; IL6; 1		
SO	SEQUENCE	207 AA; 23645 MW; ADP46E450E13A70 CRC64;	

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Query Match          13.1%, Score 143, DB 6, Length 175,
Best Local Similarity 28.7%, Pred. No. 2,4e-06;
Matches 31; Conservative 25; Mismatches 52; Indels 0; Gaps 0;

OY 37 ORNLNMLWVIDCFDLCYRTGICGIGLEPAAIFHLKLPAINDDHICGLGFNETSCIAK 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 KHRIRYLBEISALRKREIDCKSNMCCSSEALAEKNLNPMAEKEDCCFQCFRFFRCILAK 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 97 LADGFEEVLEYLKRFLTTERGKSVINVDYMELLTTLGMDIQDELINKIT 144
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 ITTGLEFEVYLEYLQNNRFESSKEQAGAVQKSTGLIQSLQKAKNLS 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
O9JHH3 PRELIMINARY: PRT: 207 AA.
AC O9JHH3:
DT 01-OCT-2000 (TRENBlrel. 15, Created)
DT 01-OCT-2000 (TRENBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TRENBlrel. 16, Last annotation update)
DE INTERLEUKIN-6.
IL 6.
GN GN
OC Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriidae; Scurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
LI D.H., Cullen J.M.;
LA

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RT   *The woodchuck interleukin-6 Gene : Cloning and Structural Analysis.
RL   Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.:
RA   LI D.H., Cullen J.M.;
RT   "Gene Structure of the woodchuck Interleukin-6.";
RL   Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AF012908; AAF34861.1; -.
DR   EMBL; AF122896; AAF28673.1; -.
DR   InterPro: IPR003573; -.
DR   InterPro: IPR003574; -.
pfam: PF00489; IL6; 1.
DR   PRINTS: PR00433; IL6CSFPGF.
DR   PRINTS: PR00434; INTERLEUKIN6.
DR   PROSITE: PS00254; INTERLEUKIN_6; 1.
DR   SMART: SM00126; IL6; 1.
SQ   SEQUENCE 207 AA; 23645 MW; AD2FF4E450E13470 CRC64;

Query Match           12.6% Score 138; DB 11; Length 207;
Best local similarity 21.0%; Pred No.9.2e-06;
Matches 43; Conservative 45; Mismatches 97; Indels 20; Gaps

QY      5 KLSLLVSGSLVSGTRGKLPDAPEFEKDILLR-----LMMLMVIDCF 50
       1 111: 11111
       2 KPFSIASIGLLIVATAPPASELIQRDGENSVTRNKPTRASGGTAQIISYLKEFEHR 61
DB      51 RDCFRGTGICGLILEPAIF--HKILPAINDDHCGILGFNETCKLKLDGFFEVEVF 108
       :::: 111: 111: 111: 111: 111: 111: 111: 111: 111: 111:
DB      62 KELCNDDEFC--ISHVAVSENNINPKMTEDGCFQGYGRNDCLVRITSGLEFOYVL 119
       :::: 111: 111: 111: 111: 111: 111: 111: 111: 111: 111:
QY      109 KELTTERF--GKSVINVDVMELTKTLGWIDQELMKLTHTYSPPKFDRCGLRGQLKY 166
       :::: 111: 111: 111: 111: 111: 111: 111: 111: 111: 111:
DB      120 RYRRKKPFGGNRRRAEIVDFSSKALIELIKOEVDPNRKIVFPSPPTANIMLLAKLESND 179
       :::: 111: 111: 111: 111: 111: 111: 111: 111: 111: 111:
QY      167 VWRHFASFVYLAAEKFAAGAVNL 191
       111 111 111 111 111 111 111 111 111 111
DB      180 MOKVMTMOLLISNFEDFLQFTLAAY 204

RESULT          9
Q28403         Q28403     PRELIMINARY;             PRT:    207 AA.
AC              O28403;
DT              01-NOV-1996 (TREMBLrel_01, Created)
DT              01-NOV-1996 (TREMBLrel_01, Last sequence update)
DT              01-MAR-2001 (TREMBLrel_16, Last annotation update)
DE              INTERLEUKIN 6 (FRAGMENT).
OS              IL-6.
SN              Enhydra lutris (Sea otter).
GC              Eukaryota; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi;
OC              Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Enhydra.
NCBI_Taxid=34882;
XX              111
RN               1
RP               SEQUENCE FROM N.A.
RA               KING D.P., Schrenzel M.D., McNight M.L., Reidarson T.H., Hanni K.D.,
RX               Stolt J.L., Ferrick D.A.;
RT               "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RL               Southern sea seal (Phoca vitulina), killer whale (Orcinus orca), and
DR               Immunogenetics 43:190-195(1996).
EMBL: I46804; AB01428.1; -.
HSSP: P05231; IL6.
InterPro: IPR003573; -.
DR               InterPro: IPR003574; -.
pfam: PF00489; IL6; 1.
PRINTS: PR00433; IL6CSFPGF.
DR               PRINTS: PR00434; INTERLEUKIN6.
PROSITE: PS00254; INTERLEUKIN_6; 1.
SMART: SM00126; IL6; 1.
NON_TER        1
FT              SEQUENCE 207 AA; 23527 MW; 729EE0CD91136DB8 CRC64;
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RESULT	9			
AC	028403	PRELIMINARY:	PRT:	207 AA.
DT	01-NOV-1996	(TREMBLrel_01, Created)		
DT	01-NOV-1996	(TREMBLrel_01, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel_16, Last annotation update)		
DE	INTERLEUKIN 6 (FRAGMENT).			
GN	IL-6.			
OS	Emhydra luteis (Sea otter).			
OC	Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Emhydra.			
OX	NCBI_TaxID=34882;			
RN	11			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=96163018; Pubmed=8575817;			
RA	King D.P., Schrenzel M.D., Mcknight M.L., Redarson T.H., Hanni K.D.,			
RA	Stolt J.L., Ferick D.A.;			
RT	"Molecular cloning and sequencing of Interleukin 6 cDNA fragments from			
RT	Southern sea otter (Emhydra luteis neireis).";			
RL	Immunogenetics 43:190-195(1996).			
DR	EMBL: L46804; AAB01428.1; "			
DR	HSSP: P05231; IL6.			
DR	InterPro: IPR003573; "			
DR	InterPro: IPR003574; "			
DR	Pfam: PF00489; IL6; 1.			
DR	PRINTS: PR00433; IL6GSPFMC.			
DR	PRINTS: PR00434; INTERLEUKIN6.			
DR	PROSITE: PS00254; INTERLEUKIN6; 1.			
DR	SMART: SM00126; IL6; 1.			
FT	NON_TER			
FT	SEQUENCE			
FT	207 AA; 23527 MW; 729EEDCD91136DB8 CRC64;			

Query Match	12.5%	Score 136.5	DB 6	Length 207
Best Local Similarity	23.7%	Pred. No. 1.3e-05		
Matches 47	Conservative 41	Mismatches 89	Indels 21	Gaps 6
Qy	12	VGSLVSGTRGKRLP-----DA-----PEFENDLLIQRILNMLWVDEECRDLQYRT 57		
Db	13	IGLLVWATFAFPYPGELGSDSDATSNRPPLTSSADKMEDEKFLIGKISALRNEMQDK 72		
Qy	58	GICKGILEPALIHLKLPAINDTDHGGLIGFERNSSCLKLADGFEFEVLEFKFLTFEFG 117		
Db	73	NKCEDSEVYLAENNLKPKLAKNDKCFOSRFQECFLRTTGLQFOIHLKTLSEVYSG 132		
Qy	118	SVINVDVWELLITLTCMDIQEELNKLITHTSP--PKEDRGLLGLQGLKYWRHFAFSFY 176		
Db	133	NKNNAHSVYISTHLLQTLR-PMNOIEVT--TPDPTDASIQALFKSQDKWLKHHTIHL 189		
Qy	177	LSAME--KFAQAGAVL 191		
Db	190	LRLLEDPLQSLPAIRIM 207		
RESULT 10				
097535				
ID	097535	PRELIMINARY:	PRT:	160 AA.
AC	097535			
DT	01-MAY-1999 (Tremblrel. 10, Created)			
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)			
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)			
DE	INTERLEUKIN-6 (FRAGMENT).			
GN	IL-6.			
OS	Actus vociferans (noisy night monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.			
OX	NCBI_Taxid=57176;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Echeverry S.J., Hernandez E., Moreno A., Patarro M.E., Murillo L.A.;			
RT	"Identification, cloning and sequencing of different interleukin genes			
RL	in 4 Aotus species.";			
DR	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF014505; AAD01531.1;			
DR	HSSP; P05231; IL6.			
DR	InterPro; IPR003573;			
DR	InterPro; IPR003574;			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GCSFPMGF.			
DR	PRINTS; PR00434; INTERLEUKIN.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
DR	SMART; SM00126; IL6; 1.			
FT	NON_TER 1			
SO	SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;			
Query Match	12.1%	Score 132;	DB 6;	Length 160;
Best Local Similarity	29.8%	Pred. No. 2.6e-05;		
Matches 28	Conservative 21	Mismatches 45;	Indels 0;	Gaps 0;
Qy	37	ORCLMMLWVDEECRDLQYRTGIGLIGLEPALIHLKLPAINDTDHGGLIGFERNSSCLK 96		
Db	55	KHIVILLEGIALRKREICRKNMCKSKKALAKENNLNPKMAKDGCGFQSGFNEETLTK 114		
Qy	97	LADGFEFEVLEFKFLTFEFGKSVINVDVWELLTK 130		
Db	115	ITTGLEFEVYLEYLQNRFFESSKQAGAVQWSTK 148		
RESULT 11				
09WV08				
ID	09WV08	PRELIMINARY:	PRT:	210 AA.
AC	09WV08;			
DT	01-NOV-1999 (Tremblrel. 12, Created)			

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DE 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE IL-6 (PRAGENET)
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT *Apa hamsters IL-6 partial cDNA.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA/8766.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR003573; -.
DR InterPro; IPR003574; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6CSFPMF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
PT NON_TER
SQ SEQUENCE 210 AA; 24060 MW; BD9319AFBB913AB3 CRC64;

Query Match 11.88; Score 129.5; DB 11; Length 210;
Best Local Similarity 24.96; Pval No. 6.4e-05;
Matches 52; Conservative 33; Mismatches 83; Indels 41; Gaps

QY 9 LLLVGLSLVSGTRGKLPDPAP---EPEKDLLIOR-----LMMMLVIDECFRD 52
Db 10 LVTLGLILLVWAT--ALPTSGVRDDEFTEDTPNRPVYTTSQGVGLVTVYRLREIYLRKE 67
QY 53 LCVRTICGK-----LLEPAALFHLKLPAINDPDHCGLIGFNETSLKTLADGFEEFVLF 108
Db 68 LCMNNGCCMDNDVYLIEN----NLELPVIOINDGCLQGTGMEICLLTGTGLDVOYVL 133
QY 109 KELTFEGKSVINVD-----VMELLTYTLGMDIOEELMLKLTTHYSPPKFRGILGR 160
Db 124 EPTYN-----NVQDNKKDKDARVIOSTIKTLSQIFKQVKGKPDKIVTPSPTSKALIMEK 176
Db 177 LESQKEMPRKTIKILILVALEEFLEVYMR 205

RESULT 12
Q9MZRI PRELIMINARY; PRT; 241 AA.
AC Q9MZRI;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN 6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN; LYMPH NODE;
RA MEDLINE=20304141; PubMed=10843729;
RT *Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus)*.
RL Cytochrome 12:555-565(2000).
DR EMBL; AF169176; AAF86660.1; -.
DR InterPro; IPR003573; -.
DR InterPro; IPR003574; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6CSFPMF.

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DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SMO0126; IL6; 1.
SQ SOURCE: 241 AA; 27021 MW; 781D32369ZC3EE97 CRC64;

Query Match 10.6%; Score 116.5; DB 6; Length 241;
Best Local Similarity 22.7%; Pred. No. 0.0014;
Matches 41; Conservative 30; Mismatches 99; Indels 11; Gaps 3;

OY 18 SGTGRKLPDAEPFCKLLIOHMMMLVDECFRDCYRTGCKILLEPAALFHLKLPAL 77
DB 37 SNTKAS-PDKLTLPRTGISRSISLETTELKREKCDIDVCMNRKELAEVNLHLRL 95
OY 78 NDTHCGLIGNETSCLKLADGFEFEVLEKFLTEFGKSVINVDV-----MELLTKT 131
DB 96 IEEQCFPANNETCLRTITSCIMEFRMLEHLOAKFRSDSEENTRVSVLKNIOHLKT 155
OY 132 LGMDIOELNLTHTYSPKPDGILGRLOGIKYVVRHAFSEVYLSAMEKFAQAVRVL 191
DB 156 L-----RRVKKNLNEATLKAFAVAVSLMENLOKNOMLKTTHFTLRGLINPLEFTLRAV 211
OY 192 D 192
DB 212 D 212

RESULT 13
OQOKR6 PRELIMINARY; PRT: 684 AA.

AC 09OKR6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73 KDA SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEPATOCYLLULAR CARCINOMA;
RA Yu S., Chen W., Pang X., Dong X., Wang H.;
RT "Homo sapiens mRNA for CPSF (cleavage and polyadenylation specificity factor) 73 kDa subunit."
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF171877; AAF00224.1; -
DR InterPro: IPR001279; -
DR Pfam: PF00753; lactamase_B.1.
SQ SEQUENCE 684 AA; 77485 MW; F8AA24EA6FB78377 CRC64;

Query Match 8.7%; Score 95; DB 4; Length 684;
Best Local Similarity 25.3%; Pred. No. 0.68;
Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILLEPAI-----FHLKLAINDTHCG-LIGFNETSCLKLADGFEFEVLEKFLTE 114
DB 58 LIDPAEIDLILSHFHL-----DHGALPWFLOKTSFKGRTPMTATATAYRWLLSD 109
OY 115 FGR-SVINVDVMEELTTLGMDIOELNLTHTYSPKPDGILGRLOGIKYVVRHAFAS 173
DB 110 YKVSINISADDM-LYTER---DLEESMDKIETINPHEVK-----EVAGIKFMCYH--A 156
OY 174 FYVLSA---MEKFAQAVRVL-----DSIPDVTPOV 201
DB 157 GHVLSAAMFMEIEIG--VKLLYTGDEFSROEDRHLMMAETIPNIKPI 200

RESULT 14
P79101 PRELIMINARY; PRT: 684 AA.
AC P79101;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN.
GN CPSF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97078155; PubMed-8929409;
RA Jenny A., Minvielle-Sebastia L., Preker P.J., Keller W.;
RT "Sequence similarity between the 73-kilodalton protein of mammalian CPSF and a subunit of yeast polyadenylation factor I."
RL Science 274:1514-1517(1996).
DR EMBL: X95906; CAA65151.1; -
DR InterPro: IPR001279; -
DR Pfam: PF00753; lactamase_B.1.
SQ SEQUENCE 684 AA; 77487 MW; 17A0CAFED2B8172E CRC64;

Query Match 8.7%; Score 95; DB 6; Length 684;
Best Local Similarity 25.3%; Pred. No. 0.68;
Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILLEPAI-----FHLKLAINDTHCG-LIGFNETSCLKLADGFEFEVLEKFLTE 114
DB 58 LIDPAEIDLILSHFHL-----DHGALPWFLOKTSFKGRTPMTATATAYRWLLSD 109
OY 115 FGR-SVINVDVMEELTTLGMDIOELNLTHTYSPKPDGILGRLOGIKYVVRHAFAS 173
DB 110 YKVSINISADDM-LYTER---DLEESMDKIETINPHEVK-----EVAGIKFMCYH--A 156
OY 174 FYVLSA---MEKFAQAVRVL-----DSIPDVTPOV 201
DB 157 GHVLSAAMFMEIEIG--VKLLYTGDEFSROEDRHLMMAETIPNIKPI 200

RESULT 15
OQOKR7 PRELIMINARY; PRT: 684 AA.

AC 09OKR7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73 KDA SUBUNIT.
GN CPSF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Wang H., Chen W., Yu S., Xie L.;
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF203969; AAF19420.1; -
DR MGD: MGI:1859328; CPSF3.
DR InterPro: IPR001279; -
DR Pfam: PF00753; lactamase_B.1.
SQ SEQUENCE 684 AA; 77528 MW; 00302767EDF076F CRC64;

Query Match 8.7%; Score 95; DB 11; Length 684;
Best Local Similarity 25.3%; Pred. No. 0.68;
Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILLEPAI-----FHLKLAINDTHCG-LIGFNETSCLKLADGFEFEVLEKFLTE 114
DB 58 LIDPAEIDLILSHFHL-----DHGALPWFLOKTSFKGRTPMTATATAYRWLLSD 109

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us-09-230-048-2.rspt

Page 7

QY 115 EGV-SYIANDVALLTKTIGMDIOEELTKTHYSPPEFGDLGGRLOGIKYAVRIFAS 173
 Db 110 YKAVNSIISADNR-LTTER-----DLESDMKLEPIINPEYK-----EVAIGKIFCYH-A 156
 QY 174 FYVLSA-----MEKFAQAVRYL-----DSIPDPTPV 201
 Db 157 GHVLSAAMFTIAG--VKLYLTGDSFROEDRIHMAALEPFIKPKPI 200

Search completed: October 4, 2001, 19:11:56
Job time: 1182 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 17:19:19 ; Search time 76.54 Seconds
(without alignments)
5020.588 Million cell updates/sec

Title: US-09-230-048-1

Perfect score: 612
Sequence: 1 ATGTGCTGCTCAAGTGTG.....CTCCTGACGTCCACGATAG 612

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT.*
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22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	612	100.0	612	19	AAV04630 Human herpesvirus
2	612	100.0	615	19	AAV54070 Kaposi sarcoma her
3	612	100.0	615	19	AAV10243 Human herpesvirus
4	612	100.0	35100	20	AAV73802 KSHV LTR DNA (nucl
5	612	100.0	137507	19	AAV19941 KSHV long unique c
6	61	10.0	555	17	AAV44359 CDNA encoding huma
7	54.6	8.9	555	17	AAV32818 Interleukin-6 codi
8	54.6	8.9	593	22	AAE63359 Human Interleukin
9	54	8.8	1260	20	AAZ09202 Human IL-6 recepto
10	53.6	8.8	564	15	AAO55689 Full length interl
11	53.6	8.8	564	15	AAO55691 Full length interl

12	53	8.7	486	21	AA257444 Human interleukin
13	53	8.7	525	15	AAO70446 Human Interleukin
14	53	8.7	555	17	AAO09977 Segment of human B
15	53	8.7	555	17	AAV44357 cDNA encoding huma
16	53	8.7	555	17	AAV44356 Human interleukin
17	53	8.7	555	17	AAV44360 Human interleukin
18	53	8.7	555	17	AAV44358 cDNA encoding huma
19	53	8.7	556	11	AAO03365 Segment of human B
20	53	8.7	561	13	AAO27479 Encodes human IL-6
21	53	8.7	561	15	AAO69903 Human Interleukin
22	53	8.7	561	16	AAO90773 Human Interleukin-
23	53	8.7	566	9	AAAN80300 Interleukin 6. A
24	53	8.7	639	10	AAAN1706 Human Interleukin-
25	53	8.7	663	18	AAV64947 Human Interleukin
26	53	8.7	1099	13	AAO25831 Plasmid pBSF2-L8.
27	53	8.7	1101	9	AAAN80966 Sequence encoding
28	53	8.7	1101	9	AAAN81517 DNA sequence of pB
29	53	8.7	1101	10	AAAN90131 Plasmid pBSF2-L8,
30	53	8.7	1101	10	AAAN90135 Human low adenosin
31	53	8.7	1101	10	AAAN90345 Human low adenosin
32	53	8.7	1102	21	AAV21360 Human low adenosin
33	53	8.7	1102	21	AAV35238 Human low adenosin
34	53	8.7	1113	21	AAV21361 Human low adenosin
35	53	8.7	1113	21	AAV35239 Human adenosine re
36	53	8.7	1139	9	AAAN80298 Interleukin 6. A
37	53	8.7	1139	10	AAAN90255 Interleukin-6. Ho
38	53	8.7	1161	9	AAAN81460 Sequence encoding
39	53	8.7	1162	11	AAO01763 BSF-2 gene for hum
40	53	8.7	1162	12	AAO11824 B cell differentia
41	53	8.7	1165	15	AAO56265 Sequence of human
42	53	8.7	1545	21	AAV70763 IL-6R/IL-6 fusion
43	53	8.7	1552	18	AAV7849 Human fusion polyp
44	53	8.7	1627	18	AAV7848 Human fusion polyp
45	53	8.7	2759	21	AAV21362 Human low adenosin

ALIGNMENTS

RESULT 1	ID	AAV04630	standard: DNA: 612 BP.
XX	AC	AAV04630:	
XX	DT	01-JUL-1998 (first entry)	
DE	DE	Human herpesvirus 8 interleukin-6 gene.	
XX	KM	ds: interleukin-6; IL-6; human herpesvirus 8; HHV8;	
KM	KM	shotgun-cloning; Antibody; diagnosis; treatment.	
XX	OS	Human herpesvirus 8.	
XX	FH	Key	Location/Qualifiers
FT	FT	CDS	1..612
FT	FT		/tag= a
FT	FT		/product= Interleukin-6
FT	FT		/note= "no stop codon given at 3'end"
XX	PN	W09803657-A1.	
XX	PD	29-JAN-1998.	
XX	XX		
XX	PF	19-JUL-1996; 96WO-EP03199.	
XX	XX		
PR	PR	19-JUL-1996; 96WO-EP03199.	
XX	XX		
PA	PA	(BEHM) BEHRING DIAGNOSTICS CMBH.	
PA	PA	(UNY) UNIV NEW YORK STATE.	
PI	PI	Albrecht J, Fleckenstein B, Friedman-Klen A, Huang Y, Neipel F.	


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Db 181 aagggtattctcagagccgcctgctatctttccatctgaaatctaccgacctcaagctact 240
      |||
OY 241 GATCACTGCGGGTTAATAGGATTTAATGAGACTAGCTGCTTAAAGCTCGCGATGAC 300
      |||
Db 241 gatcactcgggttattatgatttaagagactagctgcttaaaagctcgccatggc 300
      |||
OY 301 TTTTGTGAATTCGAGGTGTGTATTAAGTTTAAACGAGGTTTGAAGAAATCAGTGATA 360
      |||
Db 301 tttttgatttcggaggtgtgtttaaagtttaacgagagtttggaaaatcagtgata 360
      |||
OY 361 AACGTGAGCTGATGAGCTTTCAGACGAAAGACTTACGATGAGACATACGAGAAGCTC 420
      |||
Db 361 aacgtgagctgattgagcttctcagagaaaccttagagtgacatacaggaagagctc 420
      |||
OY 421 AATTAAGCTACTAAGACGCACTACAGTCCAAATTTACCGCGGTCTATTAGGAGAG 480
      |||
Db 421 aataagctgactaagaacgactacagccaccccaatttgcgcggtctattagagag 480
      |||
OY 481 CTTTCAGGACCTTAAGTATGGGTGAGACACTTTGCTTCTTTATGTTCTGAGTGCATG 540
      |||
Db 481 ctctcagggacttaagatttggtgagacacttgccttcttattgtcttgagtgcaatg 540
      |||
OY 541 GAAAGTTTGCAGTCAAGCGGTGCTTTTGTGACTCTATGCCAGACGTGACTCTGAC 600
      |||
Db 541 gaaagtttgcagtcagcggtgcgtgttcttgactctatcccaagcgtgactctgac 600
      |||
OY 601 GTCCACGATAAG 612
      |||
Db 601 gtccacgataag 612
      |||

RESULT 3
AAV10243
ID AAV10243 standard; DNA; 615 BP.
XX
AC AAV10243;
XX
DT 15-JUL-1998 (first entry)
XX
DE Human herpesvirus 8 (HHV-8) divergent locus DL-B probe 4.
XX
KW DL-B: thymidylate synthase; dihydrofolate reductase; probe: HHV-8;
KW Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
KW Kaposi's sarcoma; beta-chemokine-1like; hydrolisatlon; VIL-6; ss.
XX
OS Synthetic.
XX
OS Kaposi's sarcoma associated herpesvirus.
XX
PN WO9804284-A1.
XX
PD 05-FEB-1998.
XX
PF 24-JUL-1997; 97WO-US12931.
XX
PR 25-JUL-1996; 96US-0022591.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Hardwick JM, Hayward GS, Nicholas J, Reitz MR.
XX
DR WPI; 1998-130422/12.
XX
PT New human herpes virus gene region containing 8 open reading frames
PT - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based
PT large cell lymphoma
XX
PS Claim 4; Page 53; 84pp; English.
XX
CC The present probe was synthesised for detecting human herpesvirus-8
CC (HHV-8) divergent locus DL-B which lies between open reading frames
CC 11 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed
CC the presence of nine viral ORFs with gene products related to cellular

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CC proteins. These proteins include the thymidylate synthase (TS),
CC dihydrofolate reductase (DHFR), Bcl-2 homologue, IE-1A, IE-1B and,
CC four cytokines which include viral interleukin-6 (VIL-6), viral
CC macrophage inhibitory protein (vMIP)-1A and -1B and beta-chemokine-1like
CC (BCK) protein. The sequences of these proteins are given in
CC AAM0100-W40108. The invention claims the mentioned proteins and a
CC polynucleotide containing HHV-8 genes encoding one or more of these
CC proteins. The invention also claims that the polynucleotide and the
CC proteins may be used directly or indirectly, e.g. using antibodies to
CC the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's
CC sarcoma, Castleman's disease, multiple myeloma and body cavity based
CC large cell lymphoma (BCHL). The proteins have also been claimed to be
CC useful in screening compounds for drugs to treat HHV-8 diseases.
XX
SO Sequence 615 BP; 150 A; 129 C; 162 G; 174 T; 0 other;

Query Match 100.0%; Score 612; DB 19; Length 615;
Best Local Similarity 100.0%; Pred. No. 6, 2e-201;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGCTGCTCAAGTTGATGCTCTCTTGTGCTGCTGCTCACTGCTGATCTGAAAG 60
      |||
Db 1 atgtgctgctcaagttgattgctctcttgtgctgctgctcaactgctgattctgaag 60
      |||
OY 61 CCGGCGAAGTTCCCGGACGCCCGGACCTTTGAAAGATCTTCTCATTCAGAGACTCAT 120
      |||
Db 61 cgggcaagttcccgacgcccgacctttgaaagattctctcatctcagagactcat 120
      |||
OY 121 TGGATCCTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
      |||
Db 121 tggatcctatgagtatgattgattgattgattgattgattgattgattgattgattg 180
      |||
OY 181 AAGGATATCTAGAGCCGCGCTATTTTATGATGAAATACAGCAATCAAGGATCTACT 240
      |||
Db 181 aaggatattcagagccgcgtgctatttcatgaaatcacagccacacagagctact 240
      |||
OY 241 GATCACTGCGGGTTAATAGATTTAATAGATGAGACTAGCTGCTTAAAGCTCGCGATGAC 300
      |||
Db 241 gatcactcgggttattatgatttaagagactagctgcttaaaagctcgccatggc 300
      |||
OY 301 TTTTGTGAATTCGAGGTGTGTATTAAGTTTAAACGAGGTTTGAAGAAATCAGTGATA 360
      |||
Db 301 tttttgatttcggaggtgtgtttaaagtttaacgagagtttggaaaatcagtgata 360
      |||
OY 361 AACGTGAGCTGATGAGCTTTCAGACGAAAGACTTACGATGAGACATACGAGAAGCTC 420
      |||
Db 361 aacgtgagctgattgagcttctcagagaaaccttagagtgacatacaggaagagctc 420
      |||
OY 421 AATTAAGCTACTAAGACGCACTACAGTCCAAATTTACCGCGGTCTATTAGGAGAG 480
      |||
Db 421 aataagctgactaagaacgactacagccaccccaatttgcgcggtctattagagag 480
      |||
OY 481 CTTTCAGGACCTTAAGTATGGGTGAGACACTTTGCTTCTTTATGTTCTGAGTGCATG 540
      |||
Db 481 ctctcagggacttaagatttggtgagacacttgccttcttattgtcttgagtgcaatg 540
      |||
OY 541 GAAAGTTTGCAGTCAAGCGGTGCTTTTGTGACTCTATGCCAGACGTGACTCTGAC 600
      |||
Db 541 gaaagtttgcagtcagcggtgcgtgttcttgactctatcccaagcgtgactctgac 600
      |||
OY 601 GTCCACGATAAG 612
      |||
Db 601 gtccacgataag 612
      |||

RESULT 4
AAV3802/C
ID AAV3802 standard; DNA; 35100 BP.
XX
AC AAV3802;
XX
DT 25-FEB-1999 (first entry)

```


DE Full length interleukin-6 gene encoding FL17L L175M mutation.
 XX IL-6: carboxy terminal mutants; mutelins; proliferation;
 KW differentiation; immunotherapeutic; antinflammatory;
 KW thrombocytopenia; chemotherapy; bone marrow transplant; ss.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT mutation 523..525 /tag= a
 FT /note= "codon for Leu 175 mutated to encode Met"
 FT mutation 511..513 /tag= b
 FT /note= "codon for Phe 171 mutated to encode Leu"
 PN MO9402512-A.
 PD 03-FEB-1994.
 PF 23-JUL-1993: 93WO-US06928.
 PR 23-JUL-1992: 92US-0918181.
 PA (UYN-) UNIV NORTH CAROLINA.
 PI Fowlkes D;
 PS WPI: 1994-048796/06.
 DR P-PSDB: AAR45720.
 XX New carboxy terminal interleukin-6 mutelins - having amino acid
 PT subunits, at position 171 or 175, for use in immunotherapeutic or
 PT anti-inflammation compns.
 XX
 XX Claim 1: Fig 4: 79pp: English.
 XX
 XX The sequence shows the gene encoding full length L175M FL17L mutant
 CC interleukin 6. It has been found that mutants of IL-6 having amino
 CC acid subunits, at amino acid 171 or 175 have increased activity over
 CC the wild type sequence. The IL-6 mutelins are useful in
 CC proliferation of B cells, T cells, megakaryocytes and multi-
 CC potential haematopoietic progenitor cells and they also induce
 CC various acute phase proteins in liver cells. They are useful in
 CC immunotherapeutic and antinflammation compns. They can also be
 CC used for the treatment of patients suffering from thrombocytopenia
 CC or undergoing chemotherapy or bone marrow transplant.
 CC See also AAO55688-92.
 XX
 XX Sequence 564 BP: 184 A; 132 C; 132 G; 116 T; 0 other:
 SO
 Query Match 8.8%; Score 53.6; DB 15; Length 564;
 Best Local Similarity 45.5%; Pred. No. 2.7e-08;
 Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
 Oy 154 GACCTCTGTACCGTCACGATCTGCAAGCGTATTCTAGAGCCCGCTGATTATTTTCAT 213
 Db 127 gagaccgttaacaagaagatacgtgtgtaagaacagtaagaacacgtcgaagaacaaac 186
 Oy 214 CTGAATCTACAGCCATCAACGTACTGATCACTCGGGTTAATAGATTAAAGAACT 273
 Db 187 ctgaaccttcgaagatgctgaagaagaatgattctcaatctggtatcaatgaagaa 246
 Oy 274 AGCTGCTTAAACCTCGCCGATGCTTTTGAATTGAGCTCTGTTAAAGTTTAA 333
 Db 247 actgtctgtgtaaaatcatcacaagcctcttggaatttggaatcactagaaagtaactc 306
 Oy 334 ACAGCGAGATTGGAAATACGATGATTAACGTCGACGTCATGAGACTCTTGACGAAGAC 393
 Db 307 cagaacagatttgagagtagtgaagacaagcgaagagctgtccagatgtcgaaccaagtc 366
 Oy 394 TTAGATGGAGCATACAGAAAGCTCAATTAAGCTGACTAAGACGCACTACAGTCCACC 453

Db 367 ctgattccagttctgcagaataaaggcaaaatcctagatgcataaaccaccgccgattcca 426
 Oy 454 AAATTGACCGCGGCTTATTAGAGAGCTTACAGGACCTTAAGTATGCTGAGACACTTT 513
 Db 427 acccaaatcgcagcctctgcagaagctgcagcagacagaccagtgctgcaggaatg 486
 Oy 514 GCTTCGTTTATGTTCTGAGTCGCAATGCAAAAGTTTCAGAGTCGAACGCGTGGTTTG 573
 Db 487 acaactcatctcatctctgcagatcttgaaagaattcagcagctctccctccgctgctc 546
 RESULT 12
 ID AA57444 standard; DNA: 486 BP.
 AC AA57444;
 XX
 XX 10-APR-2000 (first entry)
 DE Human interleukin 6 DNA sequence.
 KW Recombinant human interleukin 6; rhIL-6; human; IL-6; ds.
 XX
 XX Homo sapiens.
 OS
 PN CN1203920-A.
 XX
 XX 06-JAN-1999.
 PD
 PF 12-MAY-1998: 98CN-0101871.
 PR 12-MAY-1998: 98CN-0101871.
 XX
 XX (STILL) SI L.
 PA
 PL SI L;
 DR WPI: 2000-106829/10.
 XX
 XX Producing recombinant human interleukin-6 - comprises e.g. artificial
 PT synthesis of up-stream and downstream oligonucleotide primers
 PS
 PS Example 1: Page 3; 13pp; Chinese.
 XX
 XX The present invention describes a method used for the production of
 CC recombinant human interleukin-6 (rhIL-6). The method comprises:
 CC artificial synthesis of up-stream and downstream oligonucleotide
 CC primers; using human IL-6 DNA gene as template and using the described
 CC primers to make PCR amplification; using EcoRI and BamHI to respectively
 CC enzyme-cut pBV220 plasmid and PCR amplified hIL-6 gene fragment, then
 CC using T4DNA ligase to make connection, using the formed expression
 CC plasmid to convert colibacillus, inducing and culturing the formed
 CC transformant and recovering rhIL-6 from the culture and purifying it.
 CC The protein expressed by transformant in this method can be 45% of
 CC total protein of thallus, and the purity of rhIL-6 can be above 95%.
 CC The present sequence represents hIL-6, as given in the present invention.
 XX
 SO Sequence 486 BP: 158 A; 113 C; 117 G; 98 T; 0 other;
 Oy
 Query Match 8.7%; Score 53; DB 21; Length 486;
 Best Local Similarity 46.0%; Pred. No. 4.1e-08;
 Matches 179; Conservative 0; Mismatches 210; Indels 0; Gaps 0;
 Oy 160 TGTACCGTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTATTTTCATCTGAA 219
 Db 61 tgaacaagaagtaacatgctgtaagaacaagaagcagcagcgaagaacaacacctgaac 120
 Oy 220 CTACGACCATCAACGATCTGACATCGCGGTTAATAGATTAAATGAGACTGCTGC 279
 Db 121 ctccaaagatgctcgaataaagaatgattctccaatctgattcaatgaagaagacttgc 180

QY 280 CTTTAAAGACCTGCGGATGCGTATTTGAAATTCGAGGCTGTGTTTAAGTTTAAACGACG 339
 DB 181 ctggcgaaataataatactacgctcttggagcttgaagctataactagaactccgaac 240
 QY 340 GAGTTTGAAATTCAGTATTAAGCTGAGCTCATGAGCTTCTGACGAAAGACTTTAGGA 399
 DB 241 agattgagagtagtgagagacacagccagagctgtgcaga tggatcaaaagtcctgalc 300
 QY 400 TGGGACATACGAGACGACTCAATTAAGCTGACTTAAGACGACATACAGTCCACCAATTT 459
 DB 301 cagttccctgcgcaaaaagcaagaactctgaatgcaataaccctcccgcaaccaacaa 360
 QY 460 GACCCGCGCTCTATTAGGAGCCCTTCAGGACTTAAGTATTTGGCTGACACACTTTGCTTCG 519
 DB 361 aatgcacagcctcgcagcaagctgcagacacaaacacagcgtcgcagagacatgacaact 420
 QY 520 TTTTATGTTCTGAGTGCATGAAAGATT 548
 DB 421 catcctatctcgcagcgtcttaagagatc 449

RESULT 13

AAQ70446

ID AAQ70446 standard; DNA; 525 BP.

XX AC AAQ70446;

XX DT 21-MAR-1995 (first entry)

XX DE Human Interleukin 6 (IL-6) coding sequence.

XX KW Interleukin; IL-6; chromatography; purification; isolation; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..525 /tag= a

XX FT /product= Interleukin 6.

XX PN US5338834-A.

XX PD 16-AUG-1994.

XX PF 26-JAN-1993; 93US-0009973.

XX PR 26-JAN-1993; 93US-0009973.

XX PA (ALIX) ALIEX BIPHARMACEUTICALS INC.

XX PI Williams AM;

XX PT WPI: 1994-263330/32.

XX Method for obtaining pure human Interleukin-6 - comprises 3-step
 XX purification method using chromatography techniques

XX PS Disclosure: Figure 1: 13pp; English.

XX A method for obtaining pure interleukin-6 (IL-6) comprises (a)
 XX fractionating a preparation contg human IL-6 by cation-exchange
 XX chromatography using a column comprising a cationic resin and
 XX eluting a first IL-6 sample; (b) fractionating the first IL-6 sample
 XX by hydrophobic chromatography using a column comprising a
 XX hydrophobic adsorbent and eluting from the column a second IL-6
 XX sample; (c) fractionating the second IL-6 sample by reverse phase
 XX HPLC in the presence of a cationic charge modifier; and (d)
 XX collecting pure IL-6. (Stops (a) and (b) are interchangeable). The
 XX obtained IL-6 has a purity of >98%. NOTE: This nucleotide sequence
 XX does not encode the entire amino acid sequence given in the
 XX corresponding R file (AAR60125) but encodes amino acids 10-183 of the
 XX given sequence.

SO Sequence 525 BP; 169 A; 130 C; 124 G; 102 T; 0 other;

Query Match 8.7%; Score 53; DB 15; Length 525;

Best Local Similarity 46.0%; Pred. No. 4,2e-08;

Matches 179; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 160 TTTTACCGTACCGGATGCGAAGGTATTTCTAGAGCCCGCTGTATTTTTCATCTGAAA 219
 DB 100 tgaataaagaataactatgttgaagaagcagaagaagcactgacgaaaaaacctcgaa 159
 QY 220 CTACGACCGCATACAGATACCTGATCATCGCGGTAAATAGATTAAAGACTAGCTGC 279
 DB 160 ctcccaagaatgtcgtgaagaagatgtgctcccaatcttgatccaattgagagactgc 219
 QY 280 CTTTAAAGACCTGCGGATGCGTATTTGAAATTCGAGGCTGTGTTTAAGTTTAAACGACG 339
 DB 220 ctggtgaaataataatactacgctcttggagcttgaagctataactagaactccgaac 279
 QY 340 GAGTTTGAAATTCAGTATTAAGCTGAGCTCATGAGCTTCTGACGAAAGACTTTAGGA 399
 DB 280 agattgagagtagtgagagacacagccagagctgtgcaga tggatcaaaagtcctgalc 339
 QY 400 TGGGACATACGAGACGACTCAATTAAGCTGACTTAAGACGACATACAGTCCACCAATTT 459
 DB 340 cagttccctgcgcaaaaagcaagaactctgaatgcaataaccctcccgcaaccaacaa 399
 QY 460 GACCCGCGCTCTATTAGGAGCCCTTCAGGACTTAAGTATTTGGCTGACACACTTTGCTTCG 519
 DB 400 aatgcacagcctcgcagcaagctgcagacacaaacacagcgtcgcagagacatgacaact 459
 QY 520 TTTTATGTTCTGAGTGCATGAAAGATT 548
 DB 460 catcctatctcgcagcgtcttaagagatc 488

RESULT 14

AAQ00977

ID AAQ00977 standard; DNA; 555 BP.

XX AC AAQ00977;

XX DT 18-AUG-1990 (first entry)

XX DE Segment of human B cell differentiation factor (hBDF) gene.

XX KW Human B cell differentiation factor gene (hBDF); fusion protein;

XX OS Homo sapiens.

XX PN JP02002354-A.

XX PD 08-JAN-1990.

XX PF 10-MAR-1988; 88JP-0075991.
 XX PR 10-MAR-1988; 88JP-0075991.

XX PA (TOYJ) TOSOH CORP.

XX PT WPI: 1990-053422/08.

XX DR P-PSDB; AAR05275.

XX human B cell differentiation factor gene segment -
 XX expressed e.g. as a fusion protein with human growth hormone. In
 XX transformed Escherichia cells, and used to produce B cell antibodies

XX Page 495-6; 17pp; Japanese.

XX Also new are recombinant plasmids contg. It and Escherichia
 XX microorganisms contg. the recombinant plasmids. hBDF produces B cell
 XX antibodies in humans. The recombinant plasmid efficiently amplifies it.

CC hBDF can be expressed in a transformed microorganism by fusing the hBDF
CC gene with human growth hormone. Treating this fusion protein with blood
CC clotting factor Xa produces the 3-amino acids Glu-Phe-Met (starting from
CC the N-terminal) attached to hBDF.

SQ Sequence 555 BP; 177 A; 139 C; 132 G; 107 T; 0 other;

Query Match	8.7%	Score 53;	DB 11;	Length 555;
Best Local Similarity	46.0%;	Pred. NO. 4.4e-08;		
Matches 179;	Conservative	0;	Mismatches 210;	Indels 0;

[illegible]

RESULT 15
AAT44357
ID AAT44357 standard; cDNA; 555 BP

AC	AA744357;
XX	
DT	21-JUL-1997 (first entry)

DE CDNA encoding human Interleukin 6 antagonist DFRD/W157R/D160R

KW Interleukin 6; IL-6; gp130; binding; hIL-6 DFRD; treatment;
 KW multiple myeloma; rheumatoid arthritis; lupus erythematosus;
 KN osteoporosis; ds.

OS Synthetic.

EH	Key	Location/Qualifiers
FT	CDS	1.555

PN W09634104-A1

PD 31-OCT-1996.

PF 26-APR-1996; 96WO-1700084

PR 28-APR-1995; 95IT-ORM0273

PA (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

PI Ciliberto G, Paonessa G, Savino R;

DR WPI; 1996-497635/49.

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PT New human interleukin-6 antagonists - incapable of binding gp 130,
 used for treating e.g. multiple myeloma, arthritis or osteoporosis
 XX
 PS Claim 1; Page 17-19; 30pp; English.

CC AAT44335658 encode human interleukin-6 (hIL-6) antagonists which are
CC characterised in that they are totally incapable of binding gp130.
CC Mutations were introduced into four codons in the region coding for
CC hIL-6 cloned into p77-7/IL-6/DFRD/hind, creating the following amino
CC acid substitutions: Y71D, G35F, S118R and V121D. These mutations
CC drastically reduced the biological activity of the cytokine, without
CC altering its ability to bind to the hIL-6 receptor, thus generating
CC hIL-6 DFRD (see AAM07201). To generate the claimed antagonists further
CC mutations were generated in hIL-6 DFRD by using two mutagenic primers.
CC Antagonists were generated are IL-6 DFRD/D160R (AAM07197), IL-6
CC DFRD/M157R/D160R (AAM07198) and IL-6 DFRD/T162D (AAM07199). Another hIL-6
CC antagonist (AAM07200) was generated using Sars1 as a template. The hIL-6
CC antagonists can be used for the prepn. of pharmaceutical cpds. for the
CC treatment of multiple myeloma, rheumatoid arthritis, lupus erythematosus
CC and osteoporosis.

50 Sequence 555 BP; 183 A; 141 C; 126 G; 105 T; 0 other;

Query Match	8.7%	Score 53	DB 17	Length 555
Best Local Similarity	46.08	Pred. NO. 4.4e-08		
Matches 179	Conservative	0	Mismatches 210	Indels 0
			Gaps	0

QY	160	TGACCCTGACCGGACATCTTGGAAGGATATTTCTGAGACCCGGTGCATATTTTTCATCTGAAA	219
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QY	130	TGtaaaagaagtaaaatcagtcgtgaagaacagcaaaagagcacctggcagaaanacacccctgaac	189
	111	111	111
QY	220	CTTACCGACCATCAACGATACGATACCTACCCGGGTGATATGATATTAATGACATACGCTGC	279
	111	111	111
Db	190	cttccaaagaatggcgtcaaaaaagaatgagatgcttccaaatctggatctcaaatgagagagactctgc	249
	111	111	111
QY	280	CTTAAAAACCTCGCCGATGCGCTTTTGGAAATTCGACGCTGTGTTTAACTTTTAAACGACG	339
	111	111	111
Db	250	ctgtgtaaaatcatcatcactgcgtctctctcgagcttggagtgtaactagagctactccagaac	309
	111	111	111
QY	340	GATTTTGGAAAAATTCAGTGATATAAGCTGGAGCTCATGAGACTCTGACGCAAGACCTTGAGA	399
	111	111	111
Db	310	agaatttgagaagtagtgaaggaacaagccagaagcgtctctccagaatgycagacaaagaacctgac	369
	111	111	111
QY	400	TGGAGACATCTACAGGAAGACCTCAATTAACCTACCTAACAGCCACTTAACGTCACCCCAATTT	459
	111	111	111
Db	370	cagttcttcgcagaaaaaagcaaaagaaatctctgatactcaataaccacccctggaccacaaca	429
	111	111	111
QY	460	GACCGCGGTCTTATTAGGAGAGGCTTTCAGGGACTTAAGTATTGGGTGAGACATTTTGCTTGC	519
	111	111	111
Db	430	aatgcagacgtctgtagcgaagccttcagagcaccagaccagctggctcagagacataacaact	489
	111	111	111
QY	520	TTTTTATGTTCTGAGTGCATATGGAATAAGTT	548
	111	111	111
Db	490	catctcatctcgcgcagctcttlaaaggagct	518
	111	111	111

Search completed: October 4, 2001, 18:48:23
Job time: 5344 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 16:49:19 ; Search time 1228.55 seconds
(without alignments)
7705.232 Million cell updates/sec

Title: US-09-230-048-1

Sequence: 1 ATGCTGCTGCTTCAGTGTG.....CTCCTGAGTCCACAGATAG 612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 segs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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93: gb_v46:*
94: gb_v47:*
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96: gb_v49:*
97: gb_v50:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	612	9 A68629	A68629 Sequence 1
2	612	100.0	612	59 KS073655	U73655 Kaposi's sa
3	612	100.0	615	9 AR030968	AR030968 Sequence
4	612	100.0	615	9 AR069034	AR069034 Sequence
5	612	100.0	615	59 KS067774	U67774 Kaposi's sa
6	612	100.0	6600	59 KS071365	U71365 Kaposi's sa
7	612	100.0	35100	9 AR065849	AR065849 Sequence
8	612	100.0	137508	59 KS075698	U75698 Kaposi's sa

RESULT	4	AR069034	615 bp	DNA	PAT	29-SEP-1999
LOCUS	AR069034	615 bp	DNA	PAT	29-SEP-1999	
DEFINITION	Sequence 1 from patent US 5854398.					
ACCESSION	AR069034					
VERSION	AR069034.1	GI:6001241				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 615)					
AUTHORS	Chang, Y., Bohonczy, R.A., Russo, J.J., Ekelman, I.S. and Moore, P.S.					
TITLE	Kaposi's sarcoma-associated herpesvirus (KSHV) Interleukin 6 (IL-6)					
FEATURES	and uses thereof					
source	Patent: US 5854398-A 1 29-DEC-1998;					
	Location/Qualifiers					
	1..615					
BASH COUNT	150 a	129 c	162 g	174 t		
ORIGIN						
Only Match	100.0%	Score 612:	DB 9:	Length 615:		
Best Local Similarity	100.0%	Pred. No. 1,le-175:				
Matches 612:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0		
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Db	1	ATGTGCTGGTTCAAGTTGTGTGCTCTCTCTGCTGCTCGGTTCACTGCTGATATCTGAAAGC 60				
QY	61	CGGGCCAAAGTCCCGCCGACCCCGCCGAGTTGAAAGAGATCTTCATTCATTCAGACACTCAAT 120				
Db	61	CGGGCCAAAGTCCCGCCGACCCCGCCGAGTTGAAAGAGATCTTCATTCATTCAGACACTCAAT 120				
QY	121	TGCATGCTATGGGTGATGATGAATGCTTCCGGACCTCTGTACCTACCGGACGATCTGC 180				
Db	121	TGCATGCTATGGGTGATGATGAATGCTTCCGGACCTCTGTACCTACCGGACGATCTGC 180				
QY	181	AAGGGTATTTAGAGCCCGCTGCTATTTTTCATCTGAAACATCCAGGCATCAAGACTACT 240				
Db	181	AAGGGTATTTAGAGCCCGCTGCTATTTTTCATCTGAAACATCCAGGCATCAAGACTACT 240				
QY	241	GATCAGTCCGGGTAAATAGATTTTAATGAGTACCTGCTTAAAGAGCTCCGCGATGCG 300				
Db	241	GATCAGTCCGGGTAAATAGATTTTAATGAGTACCTGCTTAAAGAGCTCCGCGATGCG 300				
QY	301	TATTTTTCGAATTCAGAGTGTGTGTTTAAAGTTTAAACGAGCGAGTTTGGAAATCACTGATA 360				
Db	301	TATTTTTCGAATTCAGAGTGTGTGTTTAAAGTTTAAACGAGCGAGTTTGGAAATCACTGATA 360				
QY	361	AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGAGGACATACAGGAAGACTC 420				
Db	361	AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGAGGACATACAGGAAGACTC 420				
QY	421	AATTAAGTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480				
Db	421	AATTAAGTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480				
QY	481	CTTCAGGAGCTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540				
Db	481	CTTCAGGAGCTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540				
QY	541	GAAAGTTCAGAGTCAAGCGGTGCTGTTTGGACTATATCCAGAGCTGACTCTCGAC 600				
Db	541	GAAAGTTCAGAGTCAAGCGGTGCTGTTTGGACTATATCCAGAGCTGACTCTCGAC 600				
QY	601	GTCACAGATTAAG 612				
Db	601	GTCACAGATTAAG 612				

KSUG67774	615 bp	DNA	VRL	/28-JUN-1997
LOCUS	KSU67774			
DEFINITION	Kaposi's sarcoma-associated herpes-like virus vIL-6 gene, complete cds.			
ACCESSION	U67774			
VERSION	U67774.1	GI:1562493		
KEYWORDS				
SOURCE	Kapoti's sarcoma-associated herpesvirus - Human herpesvirus 8.			
ORGANISM	Human herpesvirus 8 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus. 1 (bases 1 to 615)			
REFERENCE	Nicholas,J., Ruvoilo,V., Zong,J., Clufio,D., Guo,H.G., Reltz,M.S. and Hayward,G.S. A single 13-kilobase divergent locus in the Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are homologous to or related to cellular proteins <i>J. Virol.</i> 71 (3), 1963-1974 (1997) 97184526			
AUTHORS	2 (bases 1 to 615) Nichols,J., Ruvoilo,V.R., Burns,W.H., Sandford,G., Wan,X., Clufio,D., Hendrickson,S.B., Guo,H.G., Hayward,G.S. and Reltz,M.S. Kaposi's sarcoma-associated human herpesvirus-8 encodes homologies of macrophage inflammatory protein-1 and interleukin-6 <i>Nat. Med.</i> 3 (3), 287-292 (1997) 97208913			
JOURNAL MEDLINE	3 (bases 1 to 615) Nicholas,J. Direct Submission Submitted (22-AUG-1996) Johns Hopkins Oncology Center, 418 North Bond Street, Baltimore, MD 21231, USA			
TITLE	Location/Qualifiers 1..615			
FEATURES	/organism="Human herpesvirus 8" /db_xref="taxon:37296" /note="Human herpesvirus 8; Isolated from body cavity-based lymphoma" 1..615 /note="similar to Interleukin-6" /codon_start=1 /product="vIL-6" /protein_id="AAAB1701.1" /db_xref="gi:1562494" /translation="MCMFKLMSLLVGSISLVSGTSGKLDPDAPEFEKDLIQLRNLMLN VEEFYFELTEERKSVINDWELLITGLNDIOEFLNKTLTKTHYSPPKRDRLLOR LGQAKYNRRHNSRYVISASAEKAAGCAVKRVLSIDFYTPDVHDR"			
CDS				
BASE COUNT	150	a	129	c 162 g 174 t
ORIGIN				
Query Match	100.0%; Score 612; DB 59; Length 615;			
Best Local Similarity	100.0%; Pred. No. 1.le-175;			
Matches 612; Conservative 0; Mismatches 0; Indels 0; Caps 0;				
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Db	1	ATGTGTGGTTCAAAGTGTTGGTCYTCTTCTCGTGC GTTCACTGCTGAATTCTGGAACG	60	
OY	61	CCGGGCCAAGTCCCGCACCCC CGCAGTTTTAAAAGA GATCTTCTCATTCAGAGACTCYANT	120	
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OY	121	TGATATGCTATGGTGTATGATGAATAAGCTTCCG CACA CTCTGTTACGCTACCGGACTTCG	180	
Db	121	TGATATCTATGGGTATGATGAATAAGCTTCCG CACA CTCTGTTACGCTACCGGACTTCG	180	
OY	181	AAGGGTAATTCTAGAGACCGCTCTATTTTTCATCT GAACATACCAGCAGCATCAACGATTA	240	
Db	181	AAGGGTAATTC TAGAGACCGCTCTCTATTTTTCAT CTGGAACATACCAGCAGCATCAACGATTA	240	
OY	241	GATTCACCTGGCGGCTTAATAGAGATTTAATGAG AC TACGCTCTTAAAAAGCTCCGCGATGGC	300	

Db	241	GATCATCTGGGGTAAATAGATTTAATAGACTAGCTGCCTTAAAGAAGCTGGCGGATGCG	300
Qy	301	TTTTTGAATTGAGAGTGTGTTTAAGTTTAAACGACCGAGTTTGGAATAATCAGTGATA	360
Db	301	TTTTTTGAATTCGAGAGTGTGTTTAAGTTTAAACGACCGAGTTTGGAATAATCAGTGATA	360.
Qy	361	ACGTCGAGCATATGAGCTTCGACGACGACCTTAGAATGGGACATACAGGAAGACTC	420
Db	361	ACGTCGAGCATATGAGCTTCGACGACGACCTTAGAATGGGACATACAGGAAGACTC	420
Qy	421	AATTAACCTACCTTAACGACCTACAGCTCACCACCAATTTTACCGCGGTCTATTAGGGAGG	480
Db	421	AATTAACCTACCTTAACGACCTACAGCTCACCACCAATTTTACCGCGGTCTATTAGGGAGG	480
Qy	481	CTTCAGAGCACTTAAGTATTGGGTGAGACACTTTCCTCGTTTATGTCGAGTGCATG	540
Db	481	CTTCAGAGCACTTAAGTATTGGGTGAGACACTTTCCTCGTTTATGTCGAGTGCATG	540
Qy	541	GAAATTTTGACAGCTCAGCGGTGGTGTGTTTGGACCTCTATCCAGACGAGCTCCTGAC	600
Db	541	GAAATTTTGACAGCTCAGCGGTGGTGTGTTTGGACCTCTATCCAGACGAGCTCCTGAC	600
Qy	601	GTCACGATTAAG	612
Db	601	GTCACGATTAAG	612
RESULT	6		
LOCUS	KSU71365/c		
DEFINITION	KSU71365	6600 bp	DNA
VERSION	1		
KEYWORDS	U71365		
ACCESSION	U71365		
ORGANISM	Kapoli's sarcoma-associated herpesvirus - Human herpesvirus 8.		
REFERENCE	Kapoli's sarcoma-associated herpes-like virus fragment I, putative		
AUTHORS	interleukin 6, dihydrofolate reductase and thymidylate synthase		
TITLE	genes, complete cds.		
JOURNAL	Submitted (20-SEP-1996) Molecular Biophysics and Biochemistry, Yale		
	University School of Medicine, 333 Cedar Street, New Haven, CT		
	06520, USA		
FEATURES			
source	Location/Qualifiers		
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	309..1532		
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	TVVSESSVLLFRLASVASANIANGCLK11LALTLVHAGVLYPCGDLSTPCAPAP		
	IVQREVSSEGEPOFTVGTGIPVWSSNINOCYVLRPKSRILAKPRLASATTECCRA		
	RSIRLGRKHLRISTAPAOETPAWGLVATTSFSLTPAPLAFDRNPYNHETACAKAHYS		
	IPVIVSGKRIITAPLRGQVWVHNHNSYSSISPCVATVIVSHCCNDIDPLEDSEMPNPK		
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	complement(11780..2394)		
	/note="similar to human interleukin 6 (IL6)"		
	/codon_start=1		
	/product="putative interleukin 6"		

Query Match	Best Local Similarity	Matches	612; Conservative	0; Mismatches	0; Indels	0; Caps	0; ;
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2394	100.0%; Pred. No. 1.7e-175;						
61	100.0%; Score 612; DB 59; Length 6600;						
2334	100.0%; Pred. No. 1.7e-175;						
121	100.0%; Score 612; DB 59; Length 6600;						
2274	100.0%; Pred. No. 1.7e-175;						
181	100.0%; Score 612; DB 59; Length 6600;						
2214	100.0%; Pred. No. 1.7e-175;						

JOURNAL MEDLINE	Science 274 (5293), 1739-1744 (1996)
REFERENCE	6 (bases 1 to 137508)
AUTHORS	Russo,J.U., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.
TITLE	Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8)
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)
REFERENCE	7 (bases 1 to 137508)
AUTHORS	Russo,J.U., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.
TITLE	Direct Submission
JOURNAL	Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA
REFERENCE	8 (bases 1 to 137508)
AUTHORS	Russo,J.U., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA
REMARK	Sequence update by submitter
COMMENT	On May 3, 1997 this sequence version replaced gi:1718251.
FEATURES	Location/Qualifiers
SOURCE	1. 137508 /organism="Human herpesvirus 8" /db_xref="taxon:37296" /cell_line="BC-1; virally infected primary effusion lymphoma derived cell line" /note="sequence derived from overlapping lambda phage and cosmid clones isolated from libraries; A prototype sequence for the terminal repeat (TR) unit is deposited under GenBank Accession Number U75699. The left junction variant TR sequence unit immediately preceding base pair 1 of the LUR is deposited under GenBank Accession Number U75700. The remaining LUR sequence extending from this sequence to the right TR unit is not available due to difficulties in cloning and sequencing of this region"
misc_feature	1. 137508 /note="long unique region LUR" 105..974 /note="ORF K1" /codon_start=-1 /protein_id="AAC57081.1" /db_xref="GI:1718252" /translation="MFIVVCSLAVCFGLSLSLSSPNLCQGVISPPYTLTSLNA SLTISWCNTRRLILTRVYLITLACPNVCSCHROSMWIMRROPOLITLCO PSMTVTCGVVILKCSGNVYWHILPGRNDRYSQRTYTFITLMSQTECTCSNG LSRSLNRICFWACANITPETHTVSVSSFTGRLSTSLVKIILHATROVAVVKA KSTFHLVEHLVPMTLVALLIGMGLIGTITLIFAHQKQRDSNKTVPQILDVYSLND LCTDYTPQVDMY"
CDS	1142..2794 /note="ORF 4; The HVS ORF 4 homolog has alternatively spliced messages encoding membrane bound and secreted proteins; complement binding protein VCBP homolog" /codon_start=-1 /protein_id="AAC57082.1" /db_xref="GI:1718253" /translation="MAFLRQTLILMTFTWVIGQDNKCSQNTLIGRLKMSRDGDLA VGLTVELKNSGVYVARNITATCLQGTWSEPTAVCNKSSCPNGEITQNKVIFHG ODAKYGANISYVNEGYELAGREYRYCMYASQGMAMSSSPPECEKCHPRKIKN GDFPRDYEVNDVAHFECEGTYLVGPHSLACAVNNTWTSMPTCELAGCKPESYV HGYPLOGSLYELKHKOSFACNDGFLVCNITCVTEMDPLPKVCLDIDDPNN SNGRILHTRPREKNGVPORSNVTETPPKPEDTHAATCDNCEOPKILPTSEGN ETTSNITTKQLEDEKITSQPHHTSALTSMAKAKENFTKNNSTDLHISTPISOD DATSIPSVOPTNTNAPRTILSLHTEGSPNSSTSKATSIHLSHNRHVGGL YTTLNKTQLESTNRKPTNSQAKSTPRVETNHTKTSNPAISLTDSDADVQPRPEPTL PPIRPPASKNRYLEKOLVIGTLAVALTCGLITLFFHYLFFR"
CDS	3210..6611 /note="ORF 6; ss DNA binding protein ssDBP homolog; EBV BALF2 homolog" /codon_start=-1 /protein_id="AAC57083.1" /db_xref="GI:1718254" /translation="MALKGPTLEENIGSSAATPGCGYLVAVLTHNPPIGEASLLAG YPEAKVPSLPLNGHLYESDFPLNTVAVKIKIDATASVKLSYHRAIVYHNTHLEO PIPOGKLEKLCESRELRGFSFVPOAKKGMSPACPOLPCANETMAVYETEP KERLYGKILYPSQSTTPPHIGHQAQFKPLTDELDLSPSRAQELCPRYNDISRYLH DSITFTGIAQARXKDVSTVLAQERFQVNDQKIKRLVQAKPOCCASRGDGSYLAV IDSULVAGLSYGLSTIEGPQDCEVLANTDIPTEINCETPARLRALREVMHAQDLH IGAOLFANSYVLTLRLVAKLPKQNRGDAMNNSYLOLPHKNTNOSQSYNVAVGTA GPVPSALDGSYTLQHLAVASFSPHLLARMKYVAGSVITVOSTLKAQASTGRRLR APSOMDLCOGCPAVCINTLFYRMKDRPPVLSVNGDPPVYITGTAGTYNDLILN FATFEREEENPEADPKRTYTWQCONCTEKIASMGISEGDAITLIVDIPESVY FKGSIDVVEELKFTKCMKKNVFNRENIKMHIDLPACVWQACAPVFLVLYK SLTIVDIDICTSCMKEEDNDNPVAGVPSSEMIKMHIDPMTNTEKGCDCATIGGTL KIVQSMRCDLPQDADALGMRPARNOYRIKARALMPKTIKIKNTIESNGAS IQAGFMKPAROSYIVGPTMKFLALKTLTPSTKTSALTMRKIQTITKNPILPG VSGHLELQENYKASSQAEELINVLDPVTLTVAKIKLNSILRACGQTOYVAT LSCSPYQTLVPAEEYPHVILGPGSSPDEYRAKAGSVITVOSTLKAQASTGRRLR PIIVPLVAVNKYGSNGNTNVFNCANIGFSGRGVDRLNRPESYFKNNSSMLRR HVMITPLVDRLVKRIVGINSGEFAAVRSYQNTLEDNDNLPKTYVLEVPYPRP SSCASLEEDYTYIGYAVLGEVLSLSTVGOAGVDPMTAGVASYQDIIDDCQLQ FVGPEDCLIOGOSVVEELFSPSGVSLVGVKKRIASLSDLD"
CDS	6628..8715 /note="ORF 7; transport protein homolog; EBV BALF3 homolog" /codon_start=-1 /protein_id="AAC57084.1" /db_xref="GI:1718255" /translation="MAKELAAVADVASALAMDCLISVADPATLPTKSLATLTKFPOS LHTLPLRLRONAHRCQSLSLELHFRMTATMLMPRMCALAEACLOKTSIPSCIMF OHATNSVNPENFGNALTELKSLINDVETPKRLSYVCYIGSGSLBELGVLPR VGLKRLSPYGPDLVYSNLPCLECIQEVCLDIPGTSLOANLPDTRASHICTACGE PVRCGLFENELQLOLPESIPPTPCQSVNRDDELRSSLAAMDHILIEVSRSYL EISMLYNSQHSQSDATCIGDRDASHLASFTEHDAHMRKRDRLACCLEROTPRHFD CEFRDSLETPLGCGFSVSDYTESLQKCSASFQOVVYATLQALCOLEFVYRSLKL AACQNLNKGCSQESQEARQVAGGKREVEYLRAKHQELVQKVARDFKSLSDC IRHGHILISQTLGLRMSGYVMEASALQNHFLHRQITSLPMQLOLVDCPTRENSK YIKNSVICOARLGRREHVELTLEPYKLITPDLKRHTLPPSPNPTVLAQCFACMGRH OKMVASEMIMPSITPKMPTNPENQVSPENDNHIQKRAEYIRELIVSVSYKNT MERELKILTPQSGSFGPEEKPRAGLTITGLTILFFTSAPLVLDVAKTGMIFDLTALL HHLDSNNDNSQV"
CDS	8699..11236 /note="ORF 8; glycoprotein B gb homolog; EBV BALF4 homolog" /codon_start=-1 /protein_id="AAC57085.1" /db_xref="GI:1718256" /translation="MTPRSRLATLGVVILLVPCAGAAHSRDTQTSSTSPTPGSSS KAPTRGEASGPKSVDFQTRVCSASITGELRFRLEDCPDQDKHQESLILVTK KNVPHILEKVRKRIKISTVYVRLGLESALITNKLQELPPVLYIVESIMDSYOCFSS MKVANNVEENTFTRDQVNTVFLQPEGLTDNKLQELPPVLYIVESIMDSYOCFSS ITVCEIYDMDIARSAEPNRYEVETGAYTLVNASSEKTAACVPLALMTFPRSILQTVVNLN TVVYSDRGSTPQPNRIEVEGAYTLVNASSEKTAACVPLALMTFPRSILQTVVNLN FHFVANEITATFTAPLTPVANFPDITSCLSQDINTLNSKAKLASTVHPNGTQYFH TTGGVILVWQPMASINLTHAOGSGMPTSPSPSAPMTSRRKRSASTAAAGG GSTRNLSTYQLOLFAVDKLRDGINQVLELSRACRPOVDNIMAELEKINPTSMYTA IYGRVSKATFGVDAISTECINPOSSVYNHKSRLNSKDVYARPLVTFPRFLNSNL FTGDLGARNEITLNNQVETGDKQCEHTFTRRETLVTDVAYLRTINTDITSTLNT IALNLSFIQNDIFAELIYSSAKRLVASSVSVLTGSGSLVYGFINFKPLGGLMIL I DMNREFFVRDLSIEVADLQIGKTVVNASVVTGSGSLVYGFINFKPLGGLMIL I IVEIRALDILKSRRTYIQAQVAKMILYPDVBRAPPSCGATREIRINILGHHQLO QEERKADLDLKSTPSVFOFTANGLRQRLRGYKPLQSIDISPEGE"
CDS	11363..14401 /note="ORF 9; DNA polymerase homolog; EBV BALF5 homolog" /codon_start=-1 /protein_id="AAC57086.1" /db_xref="GI:1718257" /translation="MDFENFNDIPTRCGRNTVROPTPSQSTVSESTVRCVRLIPAC QTPGRGVAVADITFTPTTYQGRKRGVEFVAGETGSIMKTRSGOANRMAHSHLIFHYD

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/note="ORF 06, major ssDNA binding protein homolog"
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HIVITPLVDRLVKRVIGINSGEFAVARSQVONLEDRNLRPESYFFKNNASMLKR
SCASLTEDYVLYGPAVAGDEVLSTLSTGQAGVPYTAGVASVYDIDIDDELQF
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CDS

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HHLQSNHNSOY*

CDS

/note="ORF 08, glycoprotein B (gB) homolog"
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IAMLSTIONIDRAKEIYSSAKRLASSVPLTFEPREYNYTHRLAGLIEDLNTI
DMNERVRDLSLTVADIGICTYVNVASVYVTCGSLYMGFINIKHPIQGLMLII
IVIALIITIMLSRRRTTIAQAPVKMYIYDVYRRKRPASGATFREIINILSHHOLD
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CDS

/note="ORF 09, DNA polymerase homolog"

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FDKLVHAAVANIQCLFQNNTSATVAAVLPVLDIPVTFPP*

CDS

/note="ORF 10, herpesvirus salm1ri ORF 10 homolog,
conserved in other gamma-herpesviruses"
/codon_start=1
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/db_xref="GI:2246469"
/translation="MOTERATFILDMEITVNSCRFTCSLTGPIYRSSGDTRLRIP
FLURLIRDBHIFELVFNIDLTLCSCVAAVADANATGDNKRIRVAGVINSSEPL
GIWRGPPDPRKRAIKFICIEFLSPLEPMETTYFKGDLPRGAEETLHNSAEL
PSRTELVTGOLRSTSPRTYGFHSVPLSLFDLTFESIGEDGNPGBOLTRKYL
FTQGERIKCAVYVNTNSTACKARVARYRPTPLSRLOLMQASDPLTTPGLARVEA
VYDCEKTIPTPOETTLRLIQLFEQHAAGCAAFYIQLAETRFVSGFVLLPGKH
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CDS

/note="ORF 11, herpesvirus salm1ri ORF 11 homolog,
conserved in other gamma-herpesviruses"
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/protein_id="AAB62621.1"
/db_xref="GI:2246496"
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TVWESSSVILFRLRASVSNINIVGSLKIIILALTVHAGVYLLCGDLSTPHCARA

Query Match 99.2%; Score 607.2; DB 59; Length 13361;
Best Local Similarity 99.5%; Pred. No. 8.9e-174;
Matches 609; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGTGCTGGTCAAGTGGTGGCTCTGTGCTGGTGGTCAAGCGGTGATCTGGACG	60
Db	17856	ATGTGCTGGTCAAGTGGTGGCTCTGTGCTGGTGGTCAAGCGGTGATCTGGACG	17797
Qy	61	CGGGGCAAGTTCGCGAGCGCCCGGAGTTGAAGAATCTTTCATTCAGAGATCAAT	120
Db	17796	CGGGGCAAGTTCGCGAGCGCCCGGAGTTGAAGAATCTTTCATTCAGAGATCAAT	17737
Qy	121	TGATGCTTATGGGTATGATGAATAGCTTCGCGACCCGCTGTTACGATACCGCATCTCG	180
Db	17736	TGATGCTTATGGGTATGATGAATAGCTTCGCGACCCGCTGTTACGATACCGCATCTCG	17677
Qy	181	AAGGATATTCAGAGCCCGCTGCTATTTTTCATCTGAACATACCAAGCATCAATCT	240
Db	17676	AAGGATATTCAGAGCCCGCTGCTATTTTTCATCTGAACATACCAAGCATCAATCT	17617
Qy	241	GATCATGCGGGGTATAGATTTAATGAGACTAGCTTAAATAAAGCTCGCGGATGGC	300
Db	17616	GATCATGCGGGGTATAGATTTAATGAGACTAGCTTAAATAAAGCTCGCGGATGGC	17557
Qy	301	TTTTTTGAATTGAGAGTGTGTTTAAGTTTAAACGACGAGATTGGAAAATCAGTGATA	360
Db	17556	TTTTTTGAATTGAGAGTGTGTTTAAGTTTAAACGACGAGATTGGAAAATCAGTGATA	17497

QY 361 AACGTGACGATGAGCTTCTGACGAGACCTTAGTAGTGGGACATACAGAGACTC 420
 DB 17496 AACCTGACGCTGACGCTTCTGACGAGACCTTAGTAGTGGGACATACAGAGACTC 17437
 QY 421 AATAGCTGACTAAGACGACCTACCTGACCCCAATTTGACCGCGCTCTATTAGGAGG 480
 DB 17436 AATAGCTGACTAAGACGACCTACCTGACCCCAATTTGACCGCGCTCTATTAGGAGG 17377
 QY 481 CTTCAGGACCTAATGATGATGAGACACTTTCGCTGCTTATGTTCTGATGCAATG 540
 DB 17376 CTTCAGGACCTAATGATGATGAGACACTTTCGCTGCTTATGTTCTGATGCAATG 17317
 QY 541 GAAAGATTGACGATCAAGCGGTGCTGTTTGGACTCTATCCAGACGATGCTGAC 600
 DB 17316 GAAAGATTGACGATCAAGCGGTGCTGTTTGGACTCTATCCAGACGATGCTGAC 17257
 QY 601 GTCCACCATAG 612
 DB 17256 GTCCACCATAG 17245

RESULT 10
 A57729 555 bp DNA PAT 03-MAR-1998
 LOCUS Sequence 7 from Patent WO9634104.
 DEFINITION A57729
 ACCESSION A57729
 VERSION A57729.1 GI:3713553
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 555)
 AUTHORS Callberto,G., Savino,R. and Ponessa,G.
 TITLE CALLBERTO,G., SAVINO,R. AND PONESSA,G. THAT ARE TOTALLY INCAPABLE OF
 ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT ARE TOTALLY INCAPABLE OF
 BINDING CP 130, AND THEIR USE IN THE PREPARATION OF PHARMACEUTICAL
 COMPOUNDS

JOURNAL Patent: WO 9634104-A 7 31-OCT-1996;
 ANGELETTI P ISP RICHERCHE BIO (IT)
 FEATURES Location/Qualifiers
 SOURCE 1..555

BASE COUNT 178 a 140 c 130 g 107 t
 ORIGIN

Query Match 10.0%; Score 61; DB 9; Length 555;
 Best Local Similarity 47.3%; Pred. No. 1.4e-07;
 Matches 184; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 160 TGTACCGTACCGCATCTGCAAGGCTATTCTAGAGCCCGCTGCTATTTTCATCTGAAA 219
 DB 130 TGTAAACAAGTACATGCTGTAAGACCAAGAGCCGCGCTTCTGGAAGCTGAAAC 189
 QY 220 CTACAGCATCAACGATCTGATGTCCTGCGGCTTAATAGATTAAATGAGACTGCTG 279
 DB 190 CTTCGAAGATGCGTGAAGAAAGAGCGATGCTCTACAAAGCAATTCATAGAGAGACTTCG 249
 QY 280 CTTAAAAAGCTCCCGCATGCTTCTTGAATTCGAGGCTGCTTGAATTTTAAAGTAAAGCAGC 339
 DB 250 CTGGTGAATTCATCATCTGCTTCTTTCGAGTTTGAGGTATACCTGATACCTCCAGAAC 309
 QY 340 GAGTTTGGAAAAATCAGTGAATAAACGTCGACGTCATGAGCTTCTGACCAACACTTGAACA 399
 DB 310 ACATTTTGAAGTACTGACGAGCAAGCAGCAGCTGTCAGATGCGCAAAAGAGCTGATC 369
 QY 400 TGGGACATACAGAGAGAGCTCAATAAGCTGACTAAGAGAGCACTACAGTCCAGCCCAATTT 459
 DB 370 CAGTTTCCGCGCAAGAAAGCAAGATCTAGATCAATTAACACCCCGTACCCCAACACA 429
 QY 460 CACCGCGCTCTATTAGGAGGCTTTCAGGAGCTTAAGTATGGGTGAGACACTTTCGCTTCG 519
 DB 430 AATCCAGGCTGCTGACGAGAGCTGACGACAGAACCAAGCTGCTGACGACATGACACT 489

QY 520 TTTATGTTCTGAGTGCATGAAAAGTT 548
 DB 490 CATCTCATTTCTCCGACCTTTAAGAGATT 518

RESULT 11
 AR082470 555 bp DNA PAT 31-AUG-2000
 LOCUS Sequence 7 from patent US 5972902.
 DEFINITION AR082470
 ACCESSION AR082470
 VERSION AR082470.1 GI:10009196
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 555)
 AUTHORS Callberto,G., Savino,R. and Ponessa,G.
 TITLE DNA encoding human IL-6 receptor antagonist and protein encoded

JOURNAL Patent: US 5972902-A 7 26-OCT-1999;
 THEREBY
 FEATURES Location/Qualifiers
 SOURCE 1..555

BASE COUNT 178 a 140 c 130 g 107 t
 ORIGIN

Query Match 10.0%; Score 61; DB 9; Length 555;
 Best Local Similarity 47.3%; Pred. No. 1.4e-07;
 Matches 184; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 160 TGTACCGTACCGCATCTGCAAGGCTATTCTAGAGCCCGCTGCTATTTTCATCTGAAA 219
 DB 130 TGTAAACAAGTACATGCTGTAAGACCAAGAGCCGCGCTTCTGGAAGCTGAAAC 189
 QY 220 CTACAGCATCAACGATCTGATGTCCTGCGGCTTAATAGATTAAATGAGACTGCTG 279
 DB 190 CTTCGAAGATGCGTGAAGAAAGAGCGATGCTCTACAAAGCAATTCATAGAGAGACTTCG 249
 QY 250 CTTAAAAAGCTCCCGCATGCTTCTTGAATTCGAGGCTGCTTGAATTTTAAAGTAAAGCAGC 339
 DB 250 CTGGTGAATTCATCATCTGCTTCTTTCGAGTTTGAGGTATACCTGATACCTCCAGAAC 309
 QY 340 GAGTTTGGAAAAATCAGTGAATAAACGTCGACGTCATGAGCTTCTGACCAACACTTGAAGA 399
 DB 310 ACATTTTGAAGTACTGACGAGCAAGCAGCAGCTGTCAGATGCGCAAAAGAGCTGATC 369
 QY 400 TGGGACATACAGAGAGAGCTCAATAAGCTGACTAAGAGAGCACTACAGTCCAGCCCAATTT 459
 DB 370 CAGTTTCCGCGCAAGAAAGCAAGATCTAGATCAATTAACACCCCGTACCCCAACACA 429
 QY 460 CACCGCGCTCTATTAGGAGGCTTTCAGGAGCTTAAGTATGGGTGAGACACTTTCGCTTCG 519
 DB 430 AATCCAGGCTGCTGACGAGAGCTGACGACAGAACCAAGCTGCTGACGACATGACACT 489
 QY 520 TTTATGTTCTGAGTGCATGAAAAGTT 548
 DB 490 CATCTCATTTCTCCGACCTTTAAGAGATT 518

RESULT 12
 CEY16A 639 bp mRNA PRI 15-MAY-1996
 LOCUS Cercopithecus torquatus Interleukin 6 mRNA, complete cds.
 DEFINITION L26032
 ACCESSION L26032
 VERSION L26032.1 GI:514341
 KEYWORDS Interleukin 6.
 SOURCE Cercopithecus torquatus (Individual, isolate FVJ) cDNA to mRNA.
 ORGANISM Cercopithecus torquatus (Primate); Catarrhini; Cercopithecoidea; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.

REFERENCE	1 (bases 1 to 639)
AUTHORS	Villinger, F., Brar, S.S., Mayne, A., Chikhal, N. and Ansari, A.A.
TITLE	Comparative sequence analysis of cytokine genes from human and nonhuman primates
JOURNAL	J. Immunol. 155 (8), 3946-3954 (1995)
MEDLINE	96003435
FEATURES	location/Qualifiers
COORDINATES	1..639

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	/product="interleukin 6"		
BASE COUNT	181 a	178 c	152 g 128 t
ORIGIN			

Query Match	9.28;	Score 56.2;	DB 91;	Length 639
Best Local Similarity	46.58;	Pred. No. 4.1e-06;		
Matched 1st Contig	200			

OY	160	TGTTACCGTACCCGGCATTCGCAAGGTAATTCGTAGACCCGCGTCAATTTTCACTGAA	21.9
Db	214	TGTMAAGGAGTACATGTGTGTGACAGCACCAAAAGAGCACTGGCAAAAACACTGTAC	27.3
OY	220	CTACCAACCATCAACGATACGTGATDCTCGCGGGTTAATAGATTTAATGAGACTAGCTGC	27.9
Db	274	CTTCCCAAGATGGCTGTAAAGATGGATGCTCTCCATCTGGAATCAATGAGAGACACTTGGC	33.3
OY	280	CTTAAAAAGCTCGCGCATGGCTTTTGTGAATTCGAGGTGTGTGAATCTTTTAACGACG	33.9
Db	334	CTGGTCAAAATCATCACTAGTGGTCTTTTGGAGTTTGGAGTAACTCATGAGACTCCAGAAC	39.2
OY	340	GAGTTTGGAAATTCAGTGTAAATAAGCTGAGCTCATGTGAGCTTCTACGCAAGACCTTAGA	43.9
Db	394	AGGTTTGAGTATGTAAGGAGCAGACCCAGACCTGTGACGTGATGTCATAAAGTCTGTATC	45.2
OY	400	TGGGACATACAGGAAGAGCTCAATPAAGCTACTAAGACGCACTACAGTCCACCCAAATTT	45.9
Db	454	CACGCTCGTGAAGAAAAGGCAAAAGATCTAGATGCAATAACACCCCTGAACCAACACA	51.3
OY	460	GACCGCGGTCTATTATGAGGAGGCTTCAGAGCACTTAAGATTTGGTGAGCACTTGTCTTGC	51.9
Db	514	AATGSCACGCTGTGTACGAAGCTGAGGCAACAGACAGTGGCTGCAGGACATGACGACG	57.3
OY	520	TTTTTATGTTCTGAGTGCATGAGAAAAGTT	54.8
Db	574	CATCTCACTCTGGACGCTTTTAAGGAGTT	60.2

RESULT	13
A42034.	
LOCUS	A42034
DEFINITION	Sequence 1 from Patent WO950085Z.
ACCESSION	A42034
VERSION	A42034.1 GI:2297535
KEYWORDS	
SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 555)
TITLE	Savino,R., Lahm,A., and Ciliberto,G. A METHODOLOGY FOR SELECTING SUPERAAGONISTS AND ANTAGONISTS AND

JOURNAL SUPERAMINANTAGONISTS OF HORMONES WHOSE RECEPTOR COMPLEX INCLUDES GP 130
 PRESENT: WO 9500882-A 1 05-JAN-1995;
 ISTITUTO DI RICERCHE DI BIOLOGIA (77)
 Other publication AU 7132494 950117
 Other publication CN 112795 931129
 Other publication JP 1261787 960603
 Other publication JP 7509571P 951019.

BASE COUNT	183 a	136 c	129 g	107 t
ORIGIN				

Query Match	8.98;	Score 54.6;	DB 9;	Length 555;
Best Local Similarity	46.38;	Pred. No. 1.2e-05;		
Matches 180;	Conservative 0;	Mismatches 209;	Indels 0;	Gaps 0;

QY 160 TGTATACCGTACCCGGCATCTGCAGAGGCTATTCTAGAGCCCGCTGATTTTTCATCTGAAA 2119
 Db 130 TGTATACCAAGAGTATACATGTGTGAAGCAGCAAGAGGACATGGACAAAAACAACTGTAC 1899
 QY 220 CTACACGCCATCAAGCATATCTGATCACTGCGCGGTATATAGCATTTATAGATCTACGTCG 2779
 Db 190 CTTCACAAAGATGCGCTTCAAAAAATGATGATGCTCCAAATCTGGATCTCAATGAGAGACTTGC 2499
 QY 280 CTTTAAAAAGCTCGCCGATGGCTTTTGTGAATTGAGAGGTGTGTTTAAGTTTTTAAAGACG 3399
 Db 250 CTGTGTAAAAATCATCTACTGTGCTTTTGTGAGTTTGTAGTATACCTAGATACCTCCAGAAC 3099
 QY 340 GAGTTTTGAAAAATCACTGATTTTAAAGCTGGAGCTATGAGAGCTTCTGACGAAGCACTTGAAGA 3999
 Db 310 AGATTTTAGAGTATGTAGAGAACAAAGCCAGAGCTGTCCAGATGAGTACAAAGAGTCTGTATC 3699
 QY 400 TGGGACATACAGSAGAGGCTCAATTAAGCTGACTAAGACCGCATACAGTCCACCCAAATTT 4599
 Db 370 CAGTTCCTGCGAAAAAGCCAAAGCAATCTATAGTGCATTAACCAACCCGTGACCCAAACACA 4299
 QY 460 GACCGCGGTATATTAGGAGAGGCTTCAGAGCACTTAAGTATTTGGGTGAGACACTTTGCTTCG 5199
 Db 430 AATGCCAGCGCTGTGACGAGAGCTGGAGGCAAGAAACAGTGGCTGAGAGACTATGCAACT 4899
 QY 520 TTTTATGTCTGTAGTGCATGAAAAAGTT 548
 Db 490 CATCTCATCTGTAGATCTTTTAAAGAGTT 518

RESULT	14		
LOCUS	AS1824		
DEFINITION	AS1824	555 bp	DNA
ACCESSION	AS1824	Sequence 1 from Patent WO9618648.	PAT
VERSION	AS1824.1	GI:2304572	10-MAR-1997
KEYWORDS			
SOURCE		unidentified.	
ORGANISM		unidentified	
REFERENCE		unclassified.	
AUTHORS		1 (bases 1 to 555)	
TITLE		Caliberto,G., Savino,R., Lahm,A. and Tonlatti,C.	
JOURNAL		SUPERAGONISTS AND ANTAGONISTS OF H 1L-6, AND 3D MODELLING METHOD FOR THEIR SELECTION	
COMMENT		Patent: WO 9618648-A 1 20-JUN-1996:	
FEATURES		ANGELETTI P 1ST RICHERCHE BIO (IT)	
source		Other publication AU 4187196 960703	
		Other publication CA 2177838 960615.	
		location/Qualifiers	
		1..555	

	/UD-ALIC LACON: 32044			
BASE COUNT	182 a	136 c	129 g	107 t
ORIGIN				1 others

Query Match 8.9% Score 54.6; DB 9; Length 555;

Best Local Similarity 46.3%; Pred. No. 1.2e-05;

Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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OY 160 TCTTACCGTACCGGCTATCTGCAAGGCTATTCTAGAGCCGCGTCTATTCTTCCTGAAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 TCTTAAACAAGATACATCTGTGAAACGACGAAAGGCGCTGCGGAAAAACACCTGAAAC 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 220 CTACAGGCACTCAACGATGATGATCACTGCGGGTAAATAGATTTAATGAGACTAGCTGC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 CTTCCAAAGATGCGTGAAGAAACATGCTGCTTCCAACTGCGATTCAATGAGAGACTTGC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 280 CTTTAAAAAGCTGCCGATGCGCTTTTGAATTCGACGCTGCTTTTAACTTTTAAAGAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 CTGCTGAATAATCATCACTGCTGCTTTTGGAGTTGAGCTATACCTAGCTTACCTCAGAAC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 340 GAGTTTGGAAATACATGATTAACGTGAGCTGATGCTCTTCCAGCAAGACCTTGAACA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 310 AGATTTGAGACTAGTGAAGCAAGCCAGAGCTGCTCCAGATGATGACAAAGCTCTGATC 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 400 TGGGACATACAGGAGAGCTCAATTAAGCTGACTAGAGGCACTACAGTCCACCCAAATTT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 370 CAGTTCTGCGGAAAAAGGCAAGAAATCTAGATGCAATTAACCCCTGACCCCAACACA 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 460 GACCGCGCTCTATTAGGAGGCTTTCAGAGGCACTTAAGTATTCGCTGAGACACTTTCCTGC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 430 AATGCCAGCCTGCTGAGGAAAGCTGACAGGCAAGAACCAAGTGGCTGAGAGACATGACAACT 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 520 TTTTATGTTCTGAGTGCATGCAATGCAAAAGTT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 490 CATCTCATTTCTGAGATCTTTTAAAGAGTT 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15

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AR021247 AR021247 555 bp DNA PAT 05-DEC-1998
LOCUS AR021247
DEFINITION Sequence 1 from patent US 5789552.
ACCESSION AR021247
VERSION AR021247.1 GI:3975862
KEYWORDS
KEYWORDS
SOURCE
SOURCE
ORGANISM
ORGANISM
REFERENCE
REFERENCE 1 (bases 1 to 555)
AUTHORS Savino, R., Lahm, A. and Ciliberto, G.
TITLE Interleukin-6 receptor antagonists
JOURNAL Patent: US 5789552-A 1 04-AUG-1998;
FEATURES
FEATURES
source 1..555
BASE COUNT 183 a 136 c 129 g 107 t
ORIGIN
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Query Match 8.9% Score 54.6; DB 9; Length 555;

Best Local Similarity 46.3%; Pred. No. 1.2e-05;

Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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OY 160 TCTTACCGTACCGGCTATCTGCAAGGCTATTCTAGAGCCGCGTCTATTCTTCCTGAAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 TCTTAAACAAGATACATCTGTGAAACGACGAAAGGCGCTGCGGAAAAACACCTGAAAC 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 220 CTACAGGCACTCAACGATGATGATCACTGCGGGTAAATAGATTTAATGAGACTAGCTGC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 CTTCCAAAGATGCGTGAAGAAACATGCTGCTTCCAACTGCGATTCAATGAGAGACTTGC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 280 CTTTAAAAAGCTGCCGATGCGCTTTTGAATTCGACGCTGCTTTTAACTTTTAAAGAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 CTGCTGAATAATCATCACTGCTGCTTTTGGAGTTGAGCTATACCTAGCTTACCTCAGAAC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 340 GAGTTTGGAAATACATGATTAACGTGAGCTGATGCTCTTCCAGCAAGACCTTGAACA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 310 AGATTTGAGACTAGTGAAGCAAGCCAGAGCTGCTCCAGATGATGACAAAGCTCTGATC 369
OY 400 TGGGACATACAGGAGAGCTCAATTAAGCTGACTAGAGGCACTACAGTCCACCCAAATTT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 370 CAGTTCTGCGGAAAAAGGCAAGAAATCTAGATGCAATTAACCCCTGACCCCAACACA 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 460 GACCGCGCTCTATTAGGAGGCTTTCAGAGGCACTTAAGTATTCGCTGAGACACTTTCCTGC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 430 AATGCCAGCCTGCTGAGGAAAGCTGACAGGCAAGAACCAAGTGGCTGAGAGACATGACAACT 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 520 TTTTATGTTCTGAGTGCATGCAATGCAAAAGTT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 490 CATCTCATTTCTGAGATCTTTTAAAGAGTT 518
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Job time: 4076 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 16:10:54 ; Search time 998.49 Seconds
(without alignments)
5793.895 Million cell updates/sec

Title: US-09-230-048-1
Perfect score: 612

Sequence: 1 ATGCTGCTGCTCAGTGTGTG.....CTCCTGACGTCCACGATGAG 612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_est3:*
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117: gb_estl48:*
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254: gb_estl74:*
255: gb_estl75:*
256: gb_estl76:*
257: gb_estl77:*
258: gb_estl78:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
C 1	53.4	8.7	895	106	AL570451	AA570451	AA570451
C 2	53	8.7	788	138	BE619489	BE619489	601473037
C 3	53	8.7	1021	106	AL570370	AL570370	AL570370
C 4	52.4	8.6	971	106	AL544153	AL544153	AL544153
C 5	43.4	7.1	524	140	BE812262	BE812262	RC0-AN000C
C 6	43.4	7.1	793	135	BG548340	BG548340	602575112
C 7	43	7.0	600	167	BE439683	BE439683	HTM1-7055
C 8	42	6.9	898	140	BE789809	BE789809	601481655
C 9	41.8	6.8	617	118	AM637075	AM637075	B154409
C 10	40.8	6.7	649	140	BE786701	BE786701	601475055
C 11	40.8	6.7	1101	219	CNS04172	AL078714	Drosophila
C 12	40.2	6.6	689	250	A2829745	AA282945	2M0107M05
C 13	39.2	6.4	313	26	AV207422	AV207422	AV207422
C 14	38.8	6.3	1101	219	CNS00370	AL064465	Drosophila
C 15	38.6	6.3	266	6	AA388057	AA388057	vc686c08
C 16	38.6	6.3	326	25	AV139780	AV139780	AV139780
C 17	38.2	6.2	280	6	AA381568	AA381568	EST94686
C 18	38.2	6.2	481	109	AV087394	AV087394	AV087394
C 19	38.2	6.2	481	24	AI731501	AI731501	AI731501
C 20	38.2	6.2	517	118	AM630774	AM630774	hmt8a03
C 21	38.2	6.2	860	219	CNS0128L	AL109275	Drosophila
C 22	38.2	6.2	863	106	AL544265	AL544265	AL544265
C 23	38.2	6.2	924	140	BE789477	BE789477	601482157
C 24	38	6.2	292	126	BB112656	BB112656	BB112656
C 25	37.2	6.1	389	133	BA411023	BA411023	BA411023
C 26	37.2	6.1	302	26	AV220080	AV220080	AV220080
C 27	37.2	6.1	468	228	AQ452435	AQ452435	HS_5151_L
C 28	37	6.0	293	25	AV136471	AV136471	AV136471
C 29	36.8	6.0	264	9	AA606518	AA606518	vc686c08
C 30	36.8	6.0	334	108	AV019824	AV019824	AV019824
C 31	36.8	6.0	557	12	AA792350	AA792350	vs91e10
C 32	36.6	6.0	282	25	AV161042	AV161042	AV161042
C 33	36.6	6.0	613	156	C88575	C88575	Mou
C 34	36.4	5.9	277	109	AV079167	AV079167	AV079167
C 35	36.4	5.9	295	25	AV170382	AV170382	AV170382
C 36	36.4	5.9	431	26	AV213586	AV213586	AV213586
C 37	36.2	5.9	459	225	AQ225616	AQ225616	HS_2003_E
C 38	36.2	5.9	293	109	AV040844	AV040844	AV040844
C 39	36	5.9	281	109	AV105835	AV105835	AV105835
C 40	36	5.9	322	25	AV105835	AV105835	AV105835
C 41	35.6	5.8	281	28	AV296533	AV296533	AV296533
C 42	35.6	5.8	282	109	AV068892	AV068892	AV068892
C 43	35.4	5.8	272	109	AV095645	AV095645	AV095645
C 44	35.4	5.8	282	109	AV093279	AV093279	AV093279
C 45	35.4	5.8	284	25	AV120780	AV120780	AV120780

ALIGNMENTS

```

FEATURES
Source
1..895
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1019YP05"
/clone_1lb="LFL.NFL006.PL2"
/tissue="vector:"Placenta"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life tech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      249 a      185 c      174 g      282 t      5 others
ORIGIN

Query Match      8.7%: Score 53.4; DB 106; Length 895;
Best Local Similarity 45.5%: Pred. No. 1.2e-05;
Matches 177; Conservative 2; Mismatches 210; Indels 0; Gaps 0;

QY 160 TGTATCCGATCCGGCATCTGCAGAGGTATTCTAGACCCCGCTGCTATTCTTTCATCTGAAA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 803 TGTATCAAGAGTATCACTGTGTGTAAGACGAAAGAGAGACGACGACGACGACGACGACGAC 744

QY 220 CTACAGCCATCAACATCACTACTGATCTACAGCGCGGTTAAATAGATTATATGACTACTGCG 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 743 CTTCCAAGATGGCTGTAAAGATGATGCTTCCATCTGGATTCATATGAGAGACCTTGC 684

QY 280 CTTAAAGAGCTGCGCGATGGCTTTTGTGATTCGAGAGGTGTGTTTAAATTTTTAAAGAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 683 CTGTGTAAGATTCATCATCTGCTGCTTTTGGATTTGAGATGATTAACCTAGATACCTCCAGMNC 624

QY 340 GAGTTTGAAGATCACTGATTAACGTGACACCTCATGGAGCTTCTGACAGAGACCTTAGCA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 623 AGATTTTAGAGTAGTAGAGNCAAGCAGAGAGCTGCGAGATGAGAGTAAACAAAAGTCTCGATC 564

QY 400 TGGGACATACAGAGACAGCTCAATAGCTAGTAGACGACACTCACTCCACCAAAATT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 CAGTTCTTCGAGAAAAGGCAAAAGATCTRGATGCAATTAACACACCCCTGACCCACACACA 504

QY 460 GACCGCGCTATTATAGGAGGCTTACAGGACTTAAGATTTTGGGTGAACACTTTGCTTG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 AATGCCAGCCTGCTGACGAAGCTGCAGGACGACGAACCAAGCTGTCAGAGGACATGACAACT 444

```


Page 5

ACCESSION	H0548340
VERSION	H0548340.1
KEYWORDS	GI:13547005
SOURCE	EST.
ORGANISM	human.
REFERENCE	Human sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	NIH-MGC http://mgc.ncl.nih.gov/.
COMMENT	(bases 1 to 793) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strassburg, Ph.D. Email: cgrahbs-remail.nih.gov Tissue Procurement: Clontech Laboratories, Inc. CDNA Library Preparation: Clontech Laboratories, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LNCMI541 row: k column: 04 High quality sequence stop: 778. Location/Qualifiers 1..793 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4703355" /clone.lib="NIH_MGC_77" /lab.host="DH10B (TI phage-resistant)" /note="Organ: Lung; Vector: pNK-LIB (Clontech); Site:1: \$11 (ggcgccctgcgccc); Site:2: \$11 (ggcatatagcc); 5' adaptor sequence: 5'-CACGCGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGCCGACATG-dt(30)BN-3' (where B = A, C, G or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 215 a 210 g 197 g 171 t

ORIGIN

```

Query Match          7.1%; Score 43.4; DB 155; Length 793;
Best Local Similarity 47.6%; Pred. No. 0.016;
Matches 128; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

```

OY	160	TCGTACCCTAACCCGACTCTGCAGAGCGTTCTACAGCCCCGCTGCTATTTCATCTCGAAA	219
Db	241	TGTAACAAGAGTAACTTGCTGAAGAAGCAGCAAGCAGCAGTGGCAGAAAAAACAACCTGAC	300
OY	220	CTACAGAGCATCAAGCATCTAGTACAGCGGGTTAATAGATTATATGAGACTAGCTGC	279
Db	301	CTTCCCAAAGATGGCTCTCAAAAAGTAGTGATCTTCCCAATCTGGATTCAATGAGGAGACTTGC	360
OY	280	CTTAAAAAGCTCCGCCATGCTGCTTTTTTGAATTCAGAGTGTGTGTTAAGTTTAAACGACG	339
Db	361	CTGGTGAATAATCATCTACTGGTCTTTTGGAGTTTGAAGGTAAACCTAAGTACCTCCAGAAC	420
OY	340	CAGTTTGCAAAATACATGATTAACCTGAGACTCAGTGCAGCTTCGTGACAGAGAACCTTAAGA	399
Db	421	ACATTTGAGAGTACGTACAGAACACAGCCAGAGCTCTGCAGATGAGTACAAAAGTCCGTGATC	480
OY	400	TGGCAGCATACAGSAGAGGCTCAATAAGCT	428
Db	481	CAGTTCCTCGACAAAAAGCCAAAGAATCT	509

RESULT 7

LOCUS	DE439832	600 bp	mRNA	EST	25-JUL-2000
DEFINITION	HTM1-705R HTM1 Homo sapiens CDNA, mRNA sequence.				
ACCESSION	BE439832				

VERSION	EST.	BE439832.1	GI:9439443
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 600)		
TITLE	Gonzalez, P., Epstein, D.L. and Borres, T. Characterization of gene expression in human trabecular meshwork using single-pass sequencing of 1060 clones		
JOURNAL	Invest. Ophthalmol. Vis. Sci. (2000) In press		
COMMENT	Contact: Pedro Gonzalez Department of Ophthalmology Duke University Duke Eye Center, Tel: 919 681 4085 Fax: 919 684 8983 Email: pedro.gonzalez@duke.edu.		
FEATURES	Location/Qualifiers		
SOURCE	1..600 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="HFM1" /tissue_type="Trabecular meshwork"		
BASE COUNT	182 a 112 c 131 g 173 t		2 others
ORIGIN			
Query Match	7.0% Score 43; DB 167; Length 600;		
Best Local Similarity	46.5% Pred. No. 0.019;		
Matches 139; Conservative	0; Mismatches 160; Indels 0; Gaps		
QY	235 GAACTGATGCTACTGCGGGCTTAATAGATTAAGACTAGCTAGCTTTAAAAGCTGACC 294		
Db	2 GAATAAGATGATGATGCTCCAAATCTGANTCAAAGAGAGAGAGCTGGTGAATAATATC 61		
QY	295 GATGCTTTTTCGATTTGAGAGTGTGTTTAACTTTTAAACGACGAGTTTGGAATAATCA 354		
Db	62 ACGGCTTTTGGAGCTTTGGAGTATACCTGAGTACTCCAGAAACAGATTGAGTAGT 121		
QY	355 GTGATTAACGCTGGAGCGATGATGAGCTTCTGACGAGACCTTGAAGATGGACATACAGGA 414		
Db	122 GAGGACCAAGCCAGACGATGACAGATGACAGATGACAAAGACCTGATCCAGTTCCTGAGAA 181		
QY	415 GAGCTCAATTAAGCTGACTTAACAGCCACTACAGTCCACCCAAATTGACCGGGCTCTATA 474		
Db	182 AAGGCAAGAAATCTGATGACAAATTAACACCCCTGACCCAAACCAAAATGCCAGCTGCTG 241		
QY	475 GCGAGCGCTTCGAGGACTTAAGTATTGCTGAGACACTTTCGCTTTATGTTCTGAG 533		
Db	242 ACGAAGCTCGACGACACAGAACCCAGTGGCTGAGAGACATGACAACTCATCTCATTTCTGG 300		
RESULT	8		
LOCUS	BE789809 898 bp mRNA EST 20-OCT-2000		
DEFINITION	60148151p1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884173 5', mRNA sequence.		
ACCESSION	BE789809		
VERSION	BE789809.1 GI:10211007		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 898)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: DCTMD/DTM/Gazdar cDNA Library Preparation: Life Technologies, Inc.		

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>

Plate: L1AM9657 row: f column: 14
 High quality sequence stop: 734.
 Location/Qualifiers

FEATURES

source

```
1. 898
/organism="Homo sapiens"
/db_xref="taxon:8606"
/clone_image="3884173"
/clone_lib="NIH_MGC-68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Lung; Vector: PCMV-SPOr6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dP.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT      269 a      150 c      217 g      262 t
ORIGIN
```

Query Match
 Best Local Similarity 46.6%; Score 42; DB 140; Length 898;
 Matches 135; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

```
259 GGATTAAATGAGACTAGCTGCTTTAAAAGCTCGCGAGTGGCTTTTGAATTCAGAGTG 318
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5  GGATTCAATGAGGAGACTGCTGCTGTTGTAATAATCATCATCTGTTTGGAGTTTAAAGTA 64
319 TTGTTAAGTTTAAACGACGAGTTTGAAATTCAGATGATTAACGTGACCTCATGAGG 378
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
65  TACCTAGAGTACCTCCAGACAGATTGAGAGTAGTGAGAGAACGCCAGACTGTGCAG 124
379 CTTTGACGAGAGACCTTAGATGATGAGATACAGAGAGAGCTCATTAGCTAGCTAAAGC 438
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
439 CACTACAGTCCACCCAAATTTGACCGGCTCTATTAGAGAGCTTGACGACTTAAGTAT 498
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
185 ACCACCCCTGAGCCACACCAAAATGCGAGCTGTGACGAGTGTCGAGCAGAGAACGAG 244
499 TGGGTGACAGACCTTGTCTGTTTANGTTCTGAGTGCAATGGAAGATT 548
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
245 TGGCTGACAGACATGACATCATCTTCCTGCGACGCTTTAAGGAGTT 294
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

RESULT 9

AM637075 617 bp mRNA EST 03-APR-2000
 LOCUS B154809.v1 Blackshear/Soares normalized Xenopus egg library Xenopus
 laevis cDNA clone PBK0054A09 5', mRNA sequence.

AM637075 1 GI:7394175
 EST.

AM637075.1 GI:7394175
 EST.
 African clawed frog.
 Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 617)

Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.,
 Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman

J.W., Bonaldo, M.F., and Soares, M.B.
 The NIHES Xenopus Maternal EST Project
 Unpublished (2000)

Contact: Perry J. Blackshear

Office of Clinical Research and Laboratory of Signal Transduction

National Institute of Environmental Health Sciences

A2-05 NIHES, 101 Alexander Drive, Research Triangle Park, NC 27709,
 USA

Tel: 919 541-4899

Fax: 919 541-4571
 Email: black009@nlh.nih.gov

Clone is available through Research Genetics, Inc., 2130 Memorial

Parkway, Huntsville, AL 35901

phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email

cdna@resgen.com

DNA sequencing and analyses performed by National Institutes of

Health Intramural Sequencing Center (NISC).

PCR primers

FORWARD: TGTAAACGACGCCAGT

BACKWARD: CAGGAACGCTATGACC

Plate: 0054 row: A column: 09

Seq primer: T7 primer.

FEATURES

source

```
1. 617
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_image="PBK0054A09"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/seq_strategy="unfertilized egg"
/lab_host="DH10B"
/notes="Vector: pT73-Pac; Site:1: EcoRI; Site:2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dRII primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 x 10^5
recombinants, with average insert sizes of 1-1.5 kb."
```

BASE COUNT 220 a 109 c 110 g 178 t
 ORIGIN

Query Match
 Best Local Similarity 49.8%; Score 41.8; DB 118; Length 617;
 Matches 106; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

```
212 ATCTGAACCTACACCATCAACGATCTGATCATCGCGTTAATAGATTAAATGAGA 271
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
29  ACCTGAGCTCCCTAAATATACCACTTAAGTAGTGCTCTCTCCAGAGTTCCAAAAGA 88
427 CTAAGCTGCTTAAAGCTCCGATGCTTTTGAATCCAGGCTGTTAAAGTTT 331
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
89  ACAATGCTGATTAAGATCCACACGACCTGTGATATTGAGATCTATCTAGTCAGT 148
332 TAACGAGGAGTTGGAATCACTGATTAACGTCGACGTGAGCTTCTGAGAGA 391
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
149 TGAAGAGACTTTCAGAGTAGTAAGAAAGCACTTGGAGTCATAGAAATCAAGACAAATG 208
392 CCTTAGGATGGGACATACAGAGAGAGCTCAATA 424
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
209 TATTATACAGGGCCATTAAAGAGATGATGAAAA 241
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

RESULT 10

BE786701 649 bp mRNA EST 20-OCT-2000
 LOCUS 601475056P1 NIH_MGC-68 Homo sapiens cDNA clone IMAGE:3878244 5',
 mRNA sequence.

BE786701 1 GI:10207899
 EST.

BE786701.1 GI:10207899
 EST.

human.

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.	1 (pages 1 to 649)		
1	NH-MGC	http://mgc.ncl.nih.gov/.		
1	National Institutes of Health, Mammalian Gene Collection (MGC)			
1	Unpublished (1999)			
1	Contact: Robert Strausberg, Ph.D.			
1	Email: cga@bbs-remail.nih.gov			
1	Library Procurement: DCTD/DRP/Gazdar			
1	cDNA Library Preparation: Life Technologies, Inc.			
1	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
1	DNA Sequencing by: Incyte Genomics, Inc.			
1	Clone distribution: MGC clone distribution information can be			
1	found through the I.M.A.G.E. Consortium/LNL at:			
1	http://limage.llnl.gov			
1	Plate: LLM9641 row: 0 column: 13			
1	High quality sequence (scpi: 628.			
1	Location/Qualifiers			
1	1. 649			
1	/organism="Homo sapiens"			
1	/db_xref="taxon:9606"			
1	/clone_1ib="NH-MGC_68"			
1	/tissue_type="large cell carcinoma"			
1	/lab_host="DH10B (phage-resistant)"			
1	/note="Organ: Lung; Vector: pCMV-Sport6; Site_1: NotI;			
1	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.			
1	Average insert size 1.8 kb. Library constructed by Life			
1	Technologies."			
BASE COUNT	189 a	164 c	154 g	142 t
ORIGIN				
Query Match	6.7%	Score 40.8;	DB 140;	Length 649;
Host Local Similarity	47.3%	Pred. No. 0.097;		
Matches 123;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0
160	TGTATCCGTCACCGCATTCGCAAGGGTATTTCTAGAGCCCGCTATTTTCATCTATA	219		
111	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
237	TGTATACAGAGCTAACTGTGTGAACACAGCAAGCCAGCAGCTCGCAGAAACACCTTAC	236		
220	CTTACACCCATCAACCATATCTACCTCCCGCTTAAATGATTTTAAATGACATCTAGC	279		
111	111 111 111 111 111 111 111 111 111 111 111 111 111			
297	CTTCCCAAGATGGCTCAAAAAGATGGATCTTCCATCTGGATTCATGAGAGACTTGC	356		
280	CTTAAAGATCCGCCATGCGCTTTTGAATTCGAGCGTGTGTTAAAGTTTAAACGAGC	339		
111	111 111 111 111 111 111 111 111 111 111 111 111 111			
357	CTCGTCAAAATCATCTACTGCTCTTTTGGAGTTTGAAGATTAACCTAGATACCTTCA	416		
340	GAGTTTGGAAATCACTAGTAAATACGTTGAGCATGAGAGCTTCTGAGAGACCTTAGA	399		
111	111 111 111 111 111 111 111 111 111 111 111 111 111			
417	ACATTTTACAGTACTAGGACACAGCAGACCTGTGACATGAGTACAAAACCTCTGATC	476		
400	TTCGACATACGACAGAGCT	419		
111	111 111 111 111 111 111 111 111 111 111 111 111 111			
477	CAGTTCTCGCAAAAAGGT	496		
RESULT 11				
CNS00L72				
LOCUS	CNS00L72	1101 bp	DNA	GSS
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC:			
	BACR48P19 of RPI-98 library from Drosophila melanogaster (fruit			
	fly), genomic survey sequence.			
ACCESSION	AL078714			
VERSION	AL078714.1	GI:5102004		
KEYWORDS	GSS.			
SOURCE	Fruit fly.			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
	Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;			
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 1101)			
AUTHORS	Genoscope.			

REFERENCE	AUTHORS	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.						house mouse.	
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Fri Oct 5 10:02:06 2001

us-09-230-048-1.rst

Page 11

BASE COUNT 97 a 49 c 59 g 61 t
ORIGIN Wang¹ plasmid vector (Life Technologies). The library was constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong

Query Match	6.38;	Score 38.6;	DB 6;	Length 266;
Best Local Similarity	58.18;	Pred. No. 0.37;		
Matches 68;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;

QY 72 GCGGACGGCCCCAGTTTGAAGAAAGATCTTCTCATTCAGACACACAAATGGATGCTATG 131

Db 120 GCGGCGTGCATTCAGTTTCCATCATGATCCTCTTATTCACAAATTCACACTTGGAGACATA 61

QY 132 GGTGATTCGATGATGATCTTTCCCGGACGCTCTTACACGTACCGCATCTGCAAGGAT 188

Db 60 AGTCTTCACAGGATGCTGCTGCTGCTACATGTTGTTAGGTACTGCTTCTTGGAAGATTT 4

Search completed: October 4, 2001, 17:36:01
Job time: 5107 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:24:14 ; Search time 54.44 Seconds

(without alignments)
227.173 Million cell updates/sec

Title: US-09-230-048-2

Sequence: 1 MCFRKLMSLLVGLVSGT.....GQAVRLDSTPDVTPVDHK 204

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*

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4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*

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22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	19	AAW74570
2	1095	100.0	204	19	AAW40103
3	1095	100.0	204	19	AAW23944
4	992	90.6	185	20	AAW95015
5	188	17.2	184	17	AAW02611
6	187	17.1	184	17	AAW02610
7	185.5	16.9	184	17	AAW08477
8	184.5	16.8	184	17	AAW08476
9	184	16.8	201	9	AAW81162
10	183.5	16.8	184	17	AAW07200
11	183.5	16.8	184	19	AAW58519

12	183.5	16.8	184	20	AAW92803	Human IL-16 mutein
13	183.5	16.8	500	18	AAW36847	Human fusion polyp
14	183.5	16.8	525	18	AAW36846	Human fusion polyp
15	183	16.7	169	15	AAW77387	Human IL-6 mutant
16	183	16.7	185	15	AAW45720	Full length Interl
17	183	16.7	185	15	AAW45718	Full length Interl
18	183	16.7	211	13	AAW25279	Mutant human BCDP
19	183	16.7	212	8	AAW0238	Interferon-beta 2a
20	183	16.7	212	6	AAW0269	Recombinant Interl
21	183	16.7	212	10	AAW90047	pBSP2-L8 sequence
22	183	16.7	212	10	AAW90371	pBSP2-L8... AAP903
23	183	16.7	212	10	AAW90436	Interferon-beta-2.
24	183	16.7	212	11	AAW90469	Interleukin-6. Ho
25	183	16.7	212	11	AAW05415	Human B-cell diffe
26	183	16.7	212	14	AAW34330	IFN-beta-2a. Homo
27	183	16.7	212	14	AAW34726	Human IL-6 (for mo
28	183	16.7	212	15	AAW49041	Human Interleukin-
29	183	16.7	212	15	AAW49249	Sequence of human
30	183	16.7	212	16	AAW72317	Interferon-beta2A.
31	183	16.7	212	18	AAW35878	Human Interleukin-
32	183	16.7	212	18	AAW35843	Human Interleukin-
33	183	16.7	212	21	AAW87816	Human IL-6 protein
34	182	16.6	185	18	AAW13999	Interleukin-6 rece
35	181	16.5	179	16	AAW55334	Human Interleukin-
36	181	16.5	183	15	AAW60125	Human Interleukin-
37	181	16.5	184	9	AAW81158	Polypeptide with B
38	181	16.5	184	10	AAW94753	Sequence of varian
39	181	16.5	184	11	AAW06532	Human B-cell stimul
40	181	16.5	184	13	AAW03914	Polypeptide with h
41	181	16.5	184	13	AAW0783	Interleukin-6. A
42	181	16.5	184	15	AAW54990	Mutant Interleukin
43	181	16.5	184	15	AAW55256	Interleukin 6. Ho
44	181	16.5	184	16	AAW4659	Interleukin-6 for
45	181	16.5	184	16	AAW68623	B-cell differentia

ALIGNMENTS

RESULT 1	
AAW74570	standard; Protein: 204 AA.
XX	
AC	AAW74570;
XX	
DT	04-DEC-1998 (first entry)
XX	
DE	Kaposi sarcoma herpes-like virus/Interleukin-6.
XX	
KW	Kaposi sarcoma herpes-like virus/Interleukin-6; PCR; primer:
KW	antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
KW	monoclonal gammopathy of undetermined significance; MCDUS; malignant;
KW	Interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
KW	systemic lupus erythematosus; amplification.
XX	
OS	Synthetic.
XX	
PN	MO9635684-A2.
PD	20-AUG-1998.
XX	
PF	12-FEB-1998; 98WU-US02820.
XX	
PR	11-NOV-1997; 97US-0967504.
PR	14-FEB-1997; 97US-0800710.
XX	
PA	(BREP/) BERENSON J R.
PA	(RETT/) RETTIG M B.
PA	(VESC/) VESCIO R A.
XX	
PI	Berenson JR, Rettig MB, Vescio RA;
XX	
DR	WPI; 1998-480765/41.

DR	N-PSDB; AAV5A4070.
XX	
PT	Treatment of multiple myeloma and monoclonal myopathy with antiviral
PT	agent - active against Kaposi sarcoma virus, or with inhibitory
PT	nucleic acid or antibody against this virus
XX	
PS	Disclosure; Fig 5b; 137pp; English.
XX	
CC	This is the amino acid sequence of the Kaposi sarcoma herpes-like
CC	virus/interleukin-6, used in the method of the invention. In this
CC	method, an antiviral agent effective against Kaposi sarcoma
CC	herpes-like virus (KSHV), is used to prevent progression of MGUS to
CC	multiple myeloma or related malignancy. KHSV- and/or interleukin-6
CC	related disorders such as specifically Alzheimer's disease, multiple
CC	sclerosis, rheumatoid arthritis, systemic lupus erythematosus, CC
CC	scleroderma and malignancies of kidney or head/neck. The vaccines
CC	(comprising a KHSV-specific immunogen) is used to produce a
CC	therapeutic and/or prophylactic response.
XX	
Sequence	204 AA;
50	

Query Match	100.0%;	Score 1095;	DB 19;	Length 204;
Best local Similarity	100.0%;	Pred. No. 2.7e-118;		
Matches 204; Conservative	0;	Mismatches	0;	Indels 0; Caps 0;

QY	1	MCWFKJMSLLIVGSLVSGTGTGKPRDAPFEKXLLIQRLNMLAWIDCFPDLCYRGIC	60
Db	1	mcwfkjmsllivgslvsgtgrkprdapfefeklllqrlnmhlwvdeefidcyrgic	60
QY	61	KGLIEPAALFHLKLPAINDDHSCGLGFNETSCLKMLADGFEFEVLEKPLYTEFGSVI	120
Db	61	kglliepaalfhlklpainddhscglgfnetsoclkkmladgffefevlklfitefgsvl	120
QY	121	NDVYMLLTKTIGMIDQELKKLTKTHTSPPKTRDGLRDLGLKTKWYHNAFSTVLSAM	180
Db	121	ndvymlltktigmiqelkkltkthtspprktrdglrlglklywvthnafstvlasm	180
QY	181	EKFASGAVFLDSDIPDYRVVDHDK	204
Db	181	ekfagavflsdipdyrvvdhdk	204

RESULT	2
AAW40103	
ID	AAW40103 standard; Protein; 204 AA

AC AAW40103;

DT. 15-JUL-1998 (first entry)

Human herpesvirus 8 (HHV-8) interleukin-6.

DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8; KW

Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; VIL-6.

05 Kaposi's sarcoma associated herpesvirus.

PN WO9804284-A.1.

PD 05-FWB-1998

PF 24-JUL-1997; 97WO-US12931.

PR 25-JUL-1996; 96US-0022591.

PA (URYJO) UNIV JOHNS HOPKINS.

PI Hardwick JM, Hayward GS, Nicholas J, Reltz MR,

DR WP1; 1998-130422/12.

PT New human herpes virus gene region containing 8 open reading frames
PT - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based
PT large cell lymphoma
XX
Claim 1: Pages 59-60; 84pp; English.
PS
XX

Claim 1; Pages 59-60; 84pp; English.

The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-6. The invention claims for novel genes, which includes the viral interleukin-6 gene, found at the divergent DL-8 locus. HHV-8 divergent locus DL-8-11es between open reading frames 11 and 17. Sequencing of the HHV-8 divergent locus DL-8 revealed the presence of nine viral ORFs with gene products related to cellular proteins. These proteins include the thymidylate synthase (TS, AAM40100), dithyrosolate reductase (DHPR, see AAM40101), Bcl-2 homologue (AAM40102), IE-1A (AAM40107), IE-1B (AAM40108) and, four cytokines which include viral interleukin-6 (vIL-6, AAM40109), viral macrophage inhibitory protein (vMIP, AAM40104) and -1B (AAM40105), and beta-chemokine-like (BCC, AAM40106) protein. The invention claims the mentioned proteins and a polynucleotide containing HHV-8 genes encoding one or more of these proteins. The invention also claims that the polynucleotide and the proteins may be used directly or indirectly, e.g. using antibodies to the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's sarcoma, Castleman's disease, multiple myeloma and body cavity based large cell lymphoma (BCBL). The proteins have also been claimed to be useful in screening compounds for drugs to treat HHV-8 diseases.

SQ Sequence 204 AA:

Query Match	100.00;	Score 1095;	DB 19;	Length 204;
Best Local Similarity	100.00;	Pred. No. 2.7e-118;		
Matches 204; Conservative	0;	Mismatches	0;	Indels 0; Caps 0

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QY	1	MCWFKMSLLILVGSLLVSGTSGKRPDPAPFEKXLLIQRLLNMMILAWIDCFPDLCYRGIC	60
Db	1	mcwfksllilvgsllvsgtsgkripdpapefeklllqrlnmmlawidecfdlcyrgic	60
QY	61	KGILPEPALFHLKLPALINDTHGSLIGFNETSCLKKIADGPFEPYELKPLTTERGKSVI	120
Db	61	kgilpepaifhlklpaldndthcgligfnetscilkkIadgffepeylkpllttergksvi	120
QY	121	NVQVMMILTKTLGMIIDGELNKLKLTHTSPPKDRGILDRIDGLKYYWRNHRASPYVLSAM	180
Db	121	nvqvmmltktlgmiidgelnklklthtsppkldrglgrlgikyywrnhraspyvlsam	180
QY	181	EKFAGQAVRLVDSIDPVTROVNDK	204
Db	181	ekfaagavrvlidsipvtrovndk	204

RESULT	3
AAW23944	
ID	AAW23944 standard; Protein; 204 AA

AC AAW23944 ;

DT 30-JUN-1998 (first entry)

Human herpesvirus 8 interleukin-6.

KW interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;

XXXXXX

[illegible]

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[illegible]

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Page 2


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FT  Misc-difference 176
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FT  Misc-difference 183
FT  /note= "Q183A"
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XX  WO9618648-A1.
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XX  20-JUN-1996.
XX
XX  13-DEC-1995; 95WO-IT00216.
XX
XX  14-DEC-1994; 94IT-ORM0805.
XX
XX  (RICE-) 1ST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX  Ciliberto G, Lahm A, Savino R, Toniatti C;
XX
XX  WPI; 1996-300575/30.
XX
XX  Identifying interleukin-6 super-agonists and (super)antagonists -
XX  using a 3-dimensional model of bovine granulocyte colony stimulating
XX  factor to identify binding sites
XX
XX  Claim 8; : 26pp; English.
XX
XX  AA02610-W02612 represent human interleukin-6 (IL-6) mutants (see
XX  AA02609 for wild type sequence), with an increased specificity for the
XX  specific receptor. These sequences were identified using the method of
XX  the invention. The method comprises comparing IL-6 with the sequence of
XX  the bovine granulocyte colony stimulating factor (bc-CSF). On the basis
XX  of this comparison a 3-dimensional model of IL-6 is formulated, which
XX  allows the identification of residues that form the site of interaction
XX  with the specific receptor, and those that constitute the site of
XX  interaction with gp130. The method can be used to identify
XX  CC superagonists, antagonists, and superantagonists of IL-6. The IL-6
XX  CC superagonists identified by this method can be used for the treatment of
XX  CC thrombocytopaenia, and for the ex vivo expansion of human haematopoietic
XX  CC progenitor cells for bone marrow transplantation and gene therapy. They
XX  CC can also be used for the treatment of breast cancer, leukaemia, and
XX  CC infectious diseases or diseases connected with disorders of bone marrow
XX  CC progenitor cells. The antagonists and superantagonists identified by the
XX  CC method (see AA02610-W02612) can be used for the treatment of diseases
XX  CC characterised by the overproduction of IL-6, particularly multiple
XX  CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
XX  CC lupus erythematosus. The method can also be used to identify IL-6
XX  CC variants with a greater affinity for the specific receptor, or variants
XX  CC with a reduced or abolished affinity for gp130.
XX
XX  Sequence 184 AA:
XX
XX  Query Match 17 2%; Score 188; DB 17; Length 184;
XX  Best Local Similarity 26.2%; Prol. No. 1.1e-13;
XX  Matches 43; Conservative 38; Mismatches 83; Indels 0; Gaps 0;
XX
XX  28 PEEFKDLIQRLLMMLVNDECDFRDLRYTGICGILPEAIPAIKPAINDTHGILIG 87
XX  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  18 plaseridqlryllldglsrlrketcknmcscsksaenlnlpkmaedgyfllg 77
XX  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  88 FNTSCIAKIAQDFEFLVFKPLTTRGKSVINVDWELIKTKLDIOELINKITKTH 147
XX  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  78 fneetcvalllglllefeyleyignrlesseegaravqmslkvlqllqkkaakndalt 137
XX  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  148 YSPKFDRLGLRLOGLKWVNHFAFSFVLSAMEKFAQAVRYL 191
XX  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX  138 tpdpttnasllcklqgqgwldqmtthllrfskfeillrslral 181
XX
XX  RESULT 6

```

```

AA02610
ID  AA02610 standard; Protein; 184 AA.
XX
XX  AA02610;
XX
XX  24-FEB-1997 (first entry)
XX
XX  Interleukin-6 (Q75Y, S76I, Q175I, S176R, Q183A).
XX
XX  Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
XX  KW bovine; granulocyte colony stimulating factor; bc-CSF; receptor; gp130;
XX  KW thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis;
XX  KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
XX  KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
XX  KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  FT  Misc-difference 75
XX  /note= "Q75Y"
XX  FT  Misc-difference 76
XX  /note= "S76I"
XX  FT  Misc-difference 175
XX  /note= "Q175I"
XX  FT  Misc-difference 176
XX  /note= "S176R"
XX  FT  Misc-difference 183
XX  /note= "Q183A"
XX
XX  WO9618648-A1.
XX
XX  20-JUN-1996.
XX
XX  13-DEC-1995; 95WO-IT00216.
XX
XX  14-DEC-1994; 94IT-ORM0805.
XX
XX  (RICE-) 1ST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX  Ciliberto G, Lahm A, Savino R, Toniatti C;
XX
XX  WPI; 1996-300575/30.
XX
XX  Identifying interleukin-6 super-agonists and (super)antagonists -
XX  using a 3-dimensional model of bovine granulocyte colony stimulating
XX  factor to identify binding sites
XX
XX  Claim 8; : 26pp; English.
XX
XX  AA02610-W02612 represent human interleukin-6 (IL-6) mutants (see
XX  AA02609 for wild type sequence), with an increased specificity for the
XX  CC specific receptor. These sequences were identified using the method of
XX  CC the invention. The method comprises comparing IL-6 with the sequence of
XX  CC the bovine granulocyte colony stimulating factor (bc-CSF). On the basis
XX  CC of this comparison a 3-dimensional model of IL-6 is formulated, which
XX  CC allows the identification of residues that form the site of interaction
XX  CC with the specific receptor, and those that constitute the site of
XX  CC interaction with gp130. The method can be used to identify
XX  CC superagonists, antagonists, and superantagonists of IL-6. The IL-6
XX  CC superagonists identified by this method can be used for the treatment of
XX  CC thrombocytopaenia, and for the ex vivo expansion of human haematopoietic
XX  CC progenitor cells for bone marrow transplantation and gene therapy. They
XX  CC can also be used for the treatment of breast cancer, leukaemia, and
XX  CC infectious diseases or diseases connected with disorders of bone marrow
XX  CC progenitor cells. The antagonists and superantagonists identified by the
XX  CC method (see AA02610-W02612) can be used for the treatment of diseases
XX  CC characterised by the overproduction of IL-6, particularly multiple
XX  CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
XX  CC lupus erythematosus. The method can also be used to identify IL-6
XX  CC variants with a greater affinity for the specific receptor, or variants
XX  CC with a reduced or abolished affinity for gp130.
XX

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FT      /note= "Y31D"
FT      Misc-difference 35
FT      /note= "G35F"
FT      Misc-difference 75
FT      /note= "Q75Y"
FT      Misc-difference 76
FT      /note= "S76I"
FT      Misc-difference 118
FT      /note= "S118R"
FT      Misc-difference 121
FT      /note= "V121D"
FT      Misc-difference 175
FT      /note= "Q175I"
FT      Misc-difference 176
FT      /note= "S176R"
FT      Misc-difference 183
FT      /note= "Q183A"
XX      MO9618648-A1.
XX      20-JUN-1996.
XX      13-DEC-1995: 95MO-IT00216.
XX      14-DEC-1994: 94IT-ORM0805.
XX      (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX      Callberco G, Lahm A, Savino R, Toniatelli C;
XX      WPI: 1996-300575/30.
XX      Identifying interleukin-6 super-agonists and (super)antagonists -
XX      using a 3-dimensional model of bovine granulocyte colony stimulating
XX      factor to identify binding sites
XX      Claim 10: 26pp: English.
XX      AA008476-W08478 represent human Interleukin-6 (IL-6) mutants (see
XX      AA002609 for wild type sequence), with greater affinity for the receptor,
XX      which can be used as IL-6 antagonists and superantagonists. These
XX      sequences were identified using the method of the invention. The method
XX      comprises comparing IL-6 with the bovine granulocyte colony stimulating
XX      factor (bc-CSF) sequence. On the basis of this comparison a
XX      3-dimensional model of IL-6 is formulated, which allows the
XX      identification of residues that form the site of interaction with the
XX      specific receptor, and those that constitute the site of interaction with
XX      gp130. The method can be used to identify superagonists, antagonists,
XX      and superantagonists of IL-6. The IL-6 superagonists identified by this
XX      method can be used for the treatment of thrombocytopenia, and for the ex
XX      vivo expansion of human haematopoietic progenitor cells for bone marrow
XX      transplantation and gene therapy. They can also be used for the treat
XX      ment of breast cancer, leukemia, and infectious diseases or
XX      diseases connected with disorders of bone marrow progenitor cells. The
XX      antagonists and superantagonists identified by the method can be used for
XX      the treatment of diseases characterised by the overproduction of IL-6,
XX      particularly multiple myeloma, rheumatoid arthritis, postmenopausal
XX      osteoporosis, and systemic lupus erythematosus. The method can also be
XX      used to identify IL-6 variants with a greater affinity for the specific
XX      receptor (see AA002610-W02612), or variants with a reduced or abolished
XX      affinity for gp130.
XX      Sequence 184 AA:
SQ

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Query Match 16.8%; Score 184.5; DB 17; Length 184;

Best Local Similarity 28.0%; Pred. No. 2.8e-13;

Matches 44; Conservative 31; Mismatches 71; Indels 11; Gaps 1;

```

QY 46 IDCEFRDL-----CYRTGCGKGLLEPAALFHLKLPAINPDHCHGLGTFNFTSCL 94
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 25 idkqltdldifisairketchkmsccskaalaeennltpkmaekdcyfigfneetcl 84

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QY 95 KKLADGPEFEVLEFKLTTEFGKSVINVDWELLTKTLGMDIOELNKLTKTHSPKPD 154
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 85 vkltgltleveyleylgnrtesssegaravgmrtkdlqfqlqkxkndalttppctn 144
QY 155 RGLIGRLGKIKYVWRHIFASFVYLSAMEKFPAGQAVRVL 191
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 145 aslltklqagqwgldmtchlllrsfkelflrsrlal 181

```

RESULT 9

AA081162

ID AAP81162 standard: protein; 201 AA.

AA081162;

DT 15-OCT-1990 (first entry)

DE Polypeptide with B-cell differentiation factor (BCDF) activity.

XX B-cell differentiation factor; BCDF; cancer; autoimmune.

XX Homo sapiens.

XX EP257406-A.

XX 02-MAR-1988.

XX 06-AUG-1988: 88EP-0111409.

XX 06-AUG-1986: 86JP-0184858.

XX 27-AUG-1986: 86JP-0200433.

XX 18-DEC-1986: 86JP-0302699.

XX 13-MAY-1987: 87JP-0116332.

XX (AJIN) AJINOMOTO KK.

XX Kishimoto TM, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;

XX WPI: 1988-057698/09.

XX Purified polypeptide with B-cell differentiation factor activity -

XX useful in prodn. of antibodies for diagnosis and therapy of

XX cancers, infectious diseases etc.

XX Claim 12: Page 41: 72pp: English.

XX Peptide with BCDF activity may be used in the production and

XX repair of B-cells. It is useful in treatment of autoimmune

XX diseases, malignant tumors and may be used to influence B-cells

XX to produce Abs in vitro.

XX Sequence 201 AA:

Query Match 16.8%; Score 184; DB 9; Length 201;

Best Local Similarity 28.1%; Pred. No. 3.6e-13;

Matches 41; Conservative 31; Mismatches 74; Indels 0; Gaps 0;

```

QY 46 IDCEFRDLCYRTGCGKGLLEPAALFHLKLPAINPDHCHGLGTFNFTSCLKLDGFEFE 105
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 53 idklrctckkmsccskaalaeennltpkmaekdcyfigfneetclvltlqlefe 112
QY 106 VLKFLTEFGKSVINVDWELLTKTLGMDIOELNKLTKTHSPKFDRLGLGRGLK 165
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 113 vyleylnrtessseegaravgmrtkdlqfqlqkxkndalttppctnaslltklqagq 172
QY 166 YWVRHIFASFVYLSAMEKFPAGQAVRVL 191
  11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
DB 173 qwigdmthlllrsfkelflrsrlal 198

```

RESULT 10

AA07200

ID	AAW07200	standard; Protein; 184 AA.
XX	AAW07200;	
AC	22-JUL-1997	(first entry)
XX		
DE	Human Interleukin 6 antagonist Sant7.	
XX	Interleukin 6; IL-6; gp130; binding; hIL-6 DFRD; treatment;	
KW	multiple myeloma; rheumatoid arthritis; lupus erythematosus;	
KW	osteoporosis.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 31	/note= "Asp substituted for wild type Tyr"
FT	Misc-difference 35	/note= "Phe substituted for wild type Gly"
FT	Misc-difference 57	/note= "Leu substituted for wild type Asp"
FT	Misc-difference 59	/note= "Glu substituted for wild type Phe"
FT	Misc-difference 60	/note= "Asn substituted for wild type Trp"
FT	Misc-difference 75	/note= "Gln substituted for wild type Tyr"
FT	Misc-difference 76	/note= "Ser substituted for wild type Lys"
FT	Misc-difference 118	/note= "Arg substituted for wild type Ser"
FT	Misc-difference 175	/note= "Gln substituted for wild type Ile"
FT	Misc-difference 176	/note= "Ser substituted for wild type Arg"
FT	Misc-difference 183	/note= "Gln substituted for wild type Ala"
XX	WC634104-A1.	
XX		
PD	31-OCT-1996.	
XX		
XX	26-APR-1996;	96MO-IT00084.
XX		
PR	28-APR-1995;	95IT-OR00273.
XX		
PA	(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.	
XX		
P1	Ciliberto G, Paonessa G, Savino R;	
DR	WPI; 1996-497635/49.	
DR	N-PSDB; AAT4359.	
XX		
PT	New human interleukin-6 antagonists - incapable of binding gp 130,	
PT	used for treating e.g. multiple myeloma, arthritis or osteoporosis	
XX		
PS	claim 1; Page 21-22; 30pp; English.	
XX		
XX	The present sequence is Sant7, a human interleukin-6 (hIL-6) antagonist	
XX	Sant7 and other hIL-6 antagonists (AAW07197-199) are characterised in	
CC	that they are totally incapable of binding gp130. Mutations were	
CC	introduced into four codons in the region coding for hIL-6 cloned into	
CC	pY17-71L-6/DFRD/hind, creating the following amino acid substitutions:	
CC	Y17D, G35F, S118R and V121D. These mutations drastically reduced the	
CC	biological activity of the cytokine, without altering its ability to	
CC	bind to the hIL-6 receptor, thus generating hIL-6 DFRD (see AAW07201).	
CC	Sant7 was generated from Sant5 (contg. 5 extra amino acids: Q75Y, S76K,	
CC	Q175I, S176R and Q183A) by inserting 3 more amino acid substitutions:	
CC	L57D, G59F and N60W. The hIL-6 antagonists can be used for the prepn. of	
CC	pharmaceutical cpds. for the treatment of multiple myeloma, rheumatoid	
CC	arthritis, lupus erythematosus and osteoporosis.	
XX		
Sequence	184 AA;	

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Query Match          16.8%; Score 183.5; DB 17; Length 184;
Best Local Similarity 27.4%; Pred. No. 3, 7e-13;
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1;

QY 46 IDCECFDL-----CYPTGICGKIGLEPAALFHLKLTLPAINDTDHGILGFNETSCL 94
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 25 idkgrfdldfalsalikelcnksnmncsskeedafwnlnlpkmeakgcykgsfneetcl 84

QY 95 KKLADGFEFEFVLFKLTTFEPKSYIINDVWELTKTLGMDIQELKKLTKTTRISPKRD 154
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 85 vklttglefeyvleylgnrfesseegaravymctklidfglqkkaaknlatitpdpctn 144

QY 155 RGLLGRLOGLKYYWRHFAFVYLSAMEKPAQAVYVL 191
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 145 aslltklgaqngwldmthlllrsfkeellrsital 181

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11	RESULT
12	AAW58519
13	ID AAW58519 standard; protein; 184 AA.
14	XX
15	AC AAW58519;
16	XX
17	DT 28-AUG-1998 (first entry)
18	XX
19	DE Human Interleukin 6 mutant with superantagonist activity San7.
20	XX
21	KW Human; interleukin 6; IL-6; hIL-6; superantagonist; San7; San7;
22	KW mutant; adenoviral vector; multiple myeloma; Castleman's disease;
23	KW mesangial glomerulonephritis; osteoporosis; rheumatoid arthritis.
24	XX
25	OS Synthetic.
26	OS Homo sapiens.
27	XX
28	PD W09813383-A1.
29	XX
30	PD 02-APR-1998.
31	XX
32	PF 24-SEP-1997; 97WO-IT0021.
33	XX
34	PR 24-SEP-1996; 96IT-RM0050.
35	XX
36	PA (CNRS) CNRS CENT NAT RECH SCI.
37	PA (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
38	XX
39	PI Clilberto G, Pericaudet M, Saggio I, Savino R;
40	XX
41	WP; 1998-230636/20.
42	XX
43	PT Recombinant defective adenovirus encoding antagonistic mutant of
44	PT human interleukin-6 - is used to treat excessive production of this
45	PT cytokine and to prolong expression of therapeutic protein from
46	PT adenoviral gene therapy vectors
47	XX
48	PS Claim 4; Page -; 19pp; English.
49	XX
50	CC New recombinant defective adenovirus vector have been developed which
51	CC contain at least 1 DNA sequence encoding a mutant form of human
52	CC interleukin-6 (hIL-6), or its fragment or derivative, that has
53	CC antagonist or superantagonist activity against hIL-6. The present
54	CC sequence represents a mutant hIL-6 with superantagonist activity having
55	CC the mutations: Y10D, G35F, L57D, E59F, M60W, Q75I, S76K, S108R, V121D,
56	CC Q175I, S107R and Q183A designated San7. The DNA sequence is placed
57	CC under control of elements that provide expression in selected cell
58	CC types, particularly the Rous sarcoma virus promoter. The adenovirus
59	CC vector can be used to treat and/or prevent conditions associated with
60	CC overproduction of IL-6, specifically multiple myeloma, Castleman's
61	CC disease, mesangial glomerulonephritis, osteoporosis, Epstein Barr
62	CC positive lymphoma, rheumatoid arthritis and systemic lupus erythematosus
63	CC cells and implants are used to express a gene encoding a therapeutic
64	CC protein. The adenovirus vector can be administered by injection,
65	CC

CC preferably as a formulation containing 104-1014 (particularly 106-1010)
 CC plaque-forming units (pfu)/ml. The adenovirus vector prolongs
 CC adenovirus-mediated expression of therapeutic genes in vivo (IL-6 is the
 CC major inflammatory cytokine produced following injection of adenovirus).
 XX Sequence 184 AA:

Query Match 16.8%; Score 183.5; DB 19; Length 184;
 Best Local Similarity 27.4%; Pred. No. 3.7e-13;
 Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1;

QY 46 IDECFRL-----CYRGICKGLEPAIFHLKLPAINDTDHGCLIGNEFNSCL 94
 DB 25 ldkqlrdldlfdlsalrkctcnksnmccskedatwlnlphkmeckdgykgyfneetcl 84
 QY 95 KKLADGFEFEVLFKELTTEFGKSVINVDWMLTKTGMDIOBELNKTTHYSPKPD 154
 DB 85 vkiltgilefevyleylnrfesseeqaravgmrtkdlqglqkxknldalttppdptn 144
 QY 155 RGLLGRLOGLAKYVVRHFASFYVLSAMEKFAQAVRL 191
 DB 145 aslltklqagngwldmcthlilrskellrslral 181

RESULT 12
 AAM92803
 ID AAM92803 standard; protein; 184 AA.
 XX
 AC AAM92803;
 XX
 DT 07-MAY-1999 (first entry)
 XX
 DE Human IL-16 mutein protein.
 XX
 KW IL-16; mutein; drug-resistance; anti-tumour drug; chemotherapy; human;
 KW inhibitor; signal transduction; cytokine; gp130; prostate carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN MO9858674-A1.
 XX
 PD 30-DEC-1998.
 XX
 PP 19-JUN-1998; 98MO-IT00169.
 XX
 PR 20-JUN-1997; 97TF-RM00368.
 XX
 PA (RICE-) IST RICEACHE BIOL MOLECULAR ANGELETTI.
 XX
 PI Borsellino N, Ciliberto G, D' Alessandro N, Savino R;
 PI Tonietti C;
 XX
 DR WPI; 1999-095359/08.
 XX
 PT New composition containing a gp130 transduction inhibitor - with a
 PT chemotherapeutic drug, useful for treating cancers especially human
 PT prostate carcinoma
 XX
 PS Claim 7; Page 29; 40pp; English.
 XX
 CC This invention describes a novel pharmaceutical composition capable of
 CC reducing drug resistance to anti-tumour drugs and comprises at least
 CC one chemotherapeutic drug and at least one agent which inhibits signal
 CC transduction from a cytokine having gp130 as transducer. The invention
 CC is used to prepare anti-tumour drugs, particularly for the treatment
 CC of human prostate carcinoma. This sequence represents a human IL-16
 CC mutein which is used in the method of the invention.
 XX
 SO Sequence 184 AA;

Query Match 16.8%; Score 183.5; DB 20; Length 184;

Best Local Similarity 27.4%; Pred. No. 3.7e-13;
 Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1;

QY 46 IDECFRL-----CYRGICKGLEPAIFHLKLPAINDTDHGCLIGNEFNSCL 94
 DB 25 ldkqlrdldlfdlsalrkctcnksnmccskedatwlnlphkmeckdgykgyfneetcl 84
 QY 95 KKLADGFEFEVLFKELTTEFGKSVINVDWMLTKTGMDIOBELNKTTHYSPKPD 154
 DB 85 vkiltgilefevyleylnrfesseeqaravgmrtkdlqglqkxknldalttppdptn 144
 QY 155 RGLLGRLOGLAKYVVRHFASFYVLSAMEKFAQAVRL 191
 DB 145 aslltklqagngwldmcthlilrskellrslral 181

RESULT 13
 AAM36847
 ID AAM36847 standard; protein; 500 AA.
 XX
 AC AAM36847;
 XX
 DT 25-MAR-1998 (first entry)
 XX
 DE Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 XX
 KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..500
 FT /note= "H-IL-6 fusion polypeptide"
 FT Region 304..316
 FT /label= linker region
 FT /note= "Links together COOH-terminus of sIL-6R with
 the NH2-terminus of IL-6"

MO9732891-A2.
 XX
 PD 12-SEP-1997.
 XX
 PP 07-MAR-1997; 97MO-DE00458.
 XX
 PR 07-MAR-1996; 96DE-4008813.
 XX
 PA (ANGE-) ANCEMANDTE GENTECNOLOGIE SYSTEME GMBH.
 XX
 PI Rose-John S;
 PI
 XX
 DR WPI; 1997-470536/43.
 DR N-PSDB; AAT97849.
 XX
 PT Conjugate of two peptide(s) with mutual affinity connected by a
 PT linker - used to modulate interactions between proteins, e.g. for ex
 PT vivo expansion of human stem cells
 XX
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC This sequence represents the fusion polypeptide H-IL-6 which contains
 CC an I3 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist.

SQ Sequence 500 AA;
 Query Match 16.8%; Score 183.5; DB 18; Length 500;
 Best Local Similarity 25.4%; Pred. No. 1.4e-12;
 Matches 48; Conservative 38; Mismatches 88; Indels 15; Gaps 2;

OY 18 SGTGKLPDAP--FEKDL-----LIQRLNMLWVIDECPFDLCYRTGCKG 62
 DB 309 sg99gsvpepyppgdskdvaaphnqpltsertldkqirylldgisalrketcnksmces 368
 OY 63 ILLEPAIFHLKLPAINDTGCLIGFNETSCLKLADGFEEFVLEFKLTTEFGKSVINV 122
 DB 369 skelaennlnlpkmaekdgcfgsgfneetclvklitgylefeyleylqnrfesseeqa 428
 OY 123 DVMELTFTKIGMDIOEELNKLTKHTYSPKFDGSLGRLOGKLYWVRHSPFYVSAMEK 182
 DB 429 ravqmsltkvliqfllqkxakndaltprdpctnaslltklgaqnvldqmtchlllrstke 488
 OY 183 FAGQAVRYL 191
 DB 489 flqsslrsl 497

RESULT 14
 AAM36846
 ID AAM36846 standard; Protein; 525 AA.
 AC AAM36846;
 XX
 DT 25-MAR-1998 (first entry)
 DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.
 XX
 KM Interleukin-6; IL-6; Interleukin-6 receptor; IL-6R; ligand; conjugate;
 KM protein interaction; therapeutic; antagonist.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= signal_peptide
 FT Region /note= "H-IL-6 fusion polypeptide"
 FT /label= linker region
 FT /note= "Linker together COOH-terminus of sIL-6R with
 FT the NH2-terminus of IL-6"
 XX
 PN MO9732891-A2.
 PD 12-SEP-1997.
 XX
 PF 07-MAR-1997; 97WO-DE00458.
 XX
 PR 07-MAR-1996; 96DE-4008813.
 XX
 PA (ANCE-) ANCEMANDTE GENTECNOLOGIE SYSTEME GMBH.
 XX
 PI Rose-John S;
 DR WPI; 1997-470536/43.
 DR N-PSDB; AAT97848.
 XX
 PT Conjugate of two peptide(s) with mutual affinity connected by a
 PT linker - used to modulate interactions between proteins, e.g. for ex
 PT vivo expansion of human stem cells
 XX
 PS Disclosure; Fig 1; 19pp; German.
 CC This sequence represents the fusion polypeptide H-IL-6 which contains
 CC an 18 amino acid linker which joins the carboxy terminus of human

CC Interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC Interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist.

SQ Sequence 525 AA;
 Query Match 16.8%; Score 183.5; DB 18; Length 525;
 Best Local Similarity 25.4%; Pred. No. 1.5e-12;
 Matches 48; Conservative 38; Mismatches 88; Indels 15; Gaps 2;

OY 18 SGTGKLPDAP--FEKDL-----LIQRLNMLWVIDECPFDLCYRTGCKG 62
 DB 334 sg99gsvpepyppgdskdvaaphnqpltsertldkqirylldgisalrketcnksmces 393
 OY 63 ILLEPAIFHLKLPAINDTGCLIGFNETSCLKLADGFEEFVLEFKLTTEFGKSVINV 122
 DB 394 skelaennlnlpkmaekdgcfgsgfneetclvklitgylefeyleylqnrfesseeqa 453
 OY 123 DVMELTFTKIGMDIOEELNKLTKHTYSPKFDGSLGRLOGKLYWVRHSPFYVSAMEK 182
 DB 454 ravqmsltkvliqfllqkxakndaltprdpctnaslltklgaqnvldqmtchlllrstke 513
 OY 183 FAGQAVRYL 191
 DB 514 flqsslrsl 522

RESULT 15
 AAR77387
 ID AAR77387 standard; Protein; 169 AA.
 AC AAR77387;
 XX
 DT 17-APR-1996 (first entry)
 DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).
 XX
 KM Human interleukin-6; IL-6a mutant; increased stability;
 KM recombinant; production; deletion mutant; amino acids 5-19.
 OS Homo sapiens.
 OS JP07224097-A.
 PN 22-AUG-1995.
 PD 08-FEB-1994; 94JP-0014461.
 XX
 PF 08-FEB-1994; 94JP-0014461.
 XX
 PR 08-FEB-1994; 94JP-0014461.
 XX
 PA (ASAG) ASAHI GLASS CO LTD.
 XX
 DR WPI; 1995-325556/42.
 DR N-PSDB; AAO94342.
 XX
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural interleukin-6
 XX
 PS Claim 1; Page 10; 18pp; Japanese.
 CC AAO94342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which
 CC lacks the amino acids Gly5-Leu19 of the wild type protein. The
 CC cDNA can be used for the recombinant prodn. of IL-6a, which has
 CC increased stability compared to wild type IL-6.
 XX
 SQ Sequence 169 AA;

